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(71) Applicant (*for all designated States except US*): **COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH** [IN/IN]; Rafi Marg, New Delhi 110 001 (IN).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **VERMA, Sunil, Kumar** [IN/IN]; Centre for Cellular and Molecular Biology, Hyderabad 500 007 (IN). **SINGH, Lalji** [IN/IN]; Centre for Cellular and Molecular Biology, Hyderabad 500 007 (IN).

(74) Agent: **GABRIEL, Devadoss, Calab;** Kumaran & Sagar, 84-C, C6 Lane, (Off Central Avenue), Sainik Farms, New Delhi 110 062 (IN).

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(54) Title: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) Abstract: The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.



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UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy¹⁻⁶⁶. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (<http://www.ncbi.nlm.nih.gov>) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals⁶⁷. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics⁶⁸ blood heam analysis^{69,70} etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification⁷¹, Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity^{72,73}. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics. therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonable doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) 'MOLECULAR KIT' and (b) 'DNA CHIPS' based application to meet the requirements of above objectives.

15 SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

20 Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). These sequences were aligned using the software *Clustal X*(1.8)(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antelope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antelope cervicapra*:

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctctttcagcaatcccatacatcggtacaaacctagtaga
atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttccactttatctctccattatcattgcagccctt
accatagtacacctactgtttctccagaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac
ccctactacactatcaaaagatactctaggagctctactattaattttaaccctcatgcttctagctctattctcaccggacctgcttggag
5 acccagacaaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct
ccgatcaattcctaacaactaggagg”.

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as ‘mcb398’ and ‘mcb869’ because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398
10 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3’ end are highly conserved amongst a vast range of animal
15 species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate
20 amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers ‘mcb398’ and ‘mcb869’ invented by the applicants fulfill the objectives of invention.

25 Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using ‘BLAST software’⁷³, it indicates identity of the family, genus or species of the analyzed
30 material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers ‘mcb398’ and ‘mcb869’. The complete procedure involved in the *analyses* (the word, ‘analyses’ should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

5 **Figure 1a.** Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures⁷⁴. The DNA obtained was amplified using the primers
10 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were
15 sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in *analyses*. The sequence (328 bp)
20 revealed from 'adil.flesh' was subjected to homology search in *nr* (i.e. *non-redundant*) database of National Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis
25 revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of
30 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

5 **Figure 2** shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

10 Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

15 Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

20 **Figure 4.** Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

25 **Table 1.** List of 221 animal species used for *In-silico* analysis to design the universal primers 'mcb398' and 'mcb869'. Table also demonstrate the 'P,S scores' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

30 Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol (^SP,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol (Ψ P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

5 **Table 2.** Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species
10 listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleotide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'mito' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements
20 of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in 'nr' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170)
25 registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera paurdus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in
30 Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh" at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard '*Panthera pardus*' source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard '*Panthera pardus*' source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis⁷⁵; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-wise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software *PHYLIP* (3.5).

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in *nr* database of NCBI. It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates

5 that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

Table 12. Other animal belonging to distantly related animal species, investigated to

10 confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population

15 of a particular species according to its demographic distributions⁷⁵. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI¹⁻⁶⁵. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal

20 by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by

25 aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed in Table 1. These sequences are publicly available in NCBI DNA databases. These sequences were aligned using the software *CLUSTAL X* (1.8). As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the

30 nucleotides between 398 to 869 in *Antelope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*)) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatatcggtacaaacctagtaga
 5 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttcactttatcctccatttatcattgcagccctt
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaaatccatccac
 ccctactacactatcaaagatatcctaggagctctactattaatttaaccctcatgcttctagtcttattctcaccggacctgcttgag
 acccagacaactataaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcaatcct
 ccgatcaattcctaacaactaggagg

10 Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked
 15 with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
20 'mcb398'	“TACCATGAGGACAAATATCATTCTG”
'mcb869'	“CCTCCTAGTTTGTTAGGGATTGATCG”

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the
 25 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually. . We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify* (1.2). The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for
 30 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were

5 *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S

10 score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataaggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed

15 in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869',

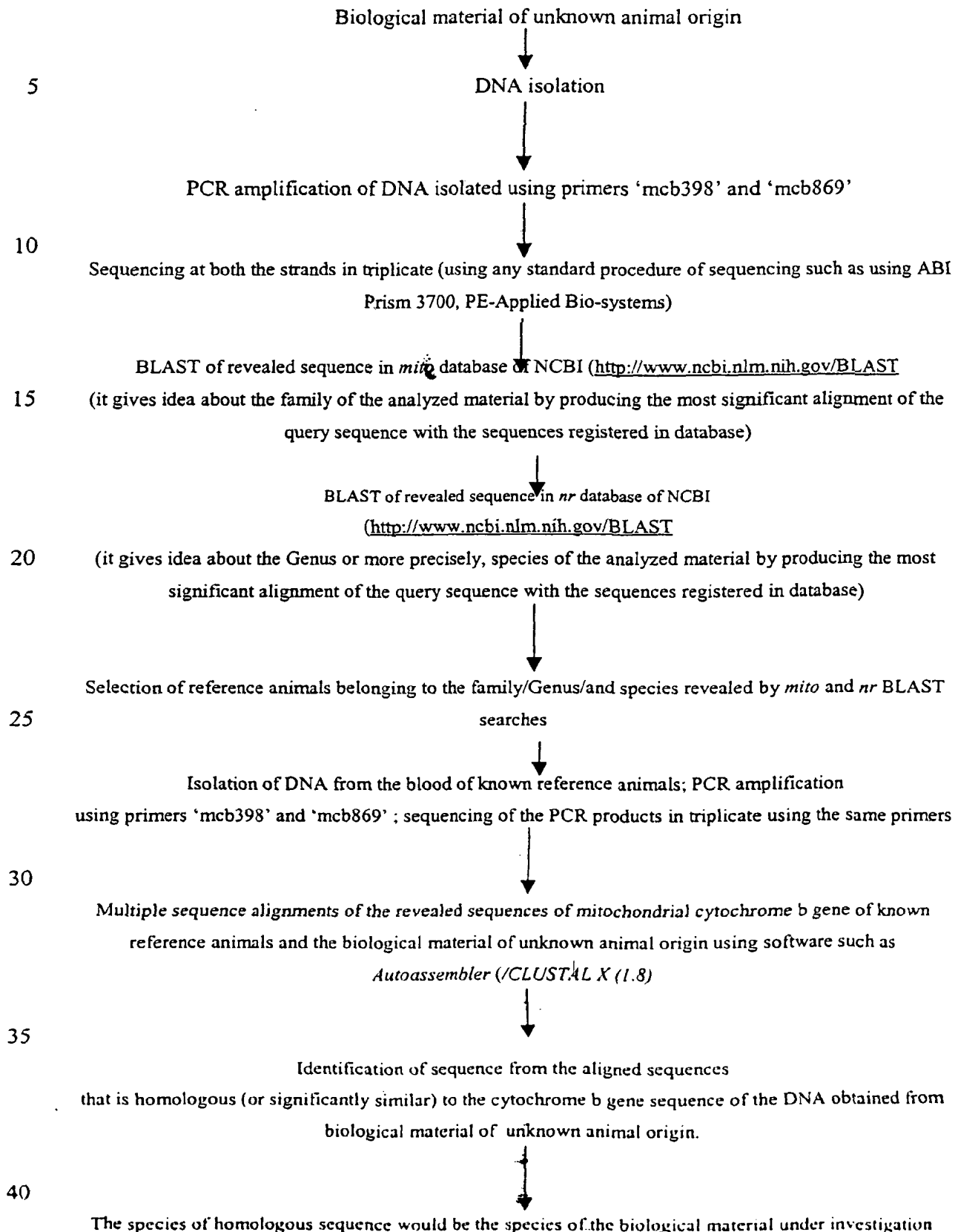
20 respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb

25 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

30 Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398' and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'



Examples

Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading
5 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources¹⁻⁶⁵. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr*
10 and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species
15 with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated from any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using
20 software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (<http://www.ncbi.nlm.nih.gov>). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

25 As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are
30 characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatcttttgaggagcaacagtcacccaatctcctttcagcaatcccatacatcggtacaaacctagtaga
 atgaatctgaggagggttctcagtagataaagcaacccttaccgatttttcgcttccactttatcctcccatttatcattgcagccctt
 accatagtacacctactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaaattccattccac
 ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcttattctcaccggacctgcttggag
 5 acccagacaactatacaccagcaaaccacttaatacacccccacatatcaagcccgaatgatacttctatttgcatacgcgaatcct
 ccgatcaattcctaacaaactaggagg”

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The t_m (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.

8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTAGGGATTGATCG"

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

- 1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.
- 20 2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.
3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.
- 25 4. The universal conditions mentioned above are:

Amplification reactions should be carried out in 20 µl reaction volume containing approximately 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.

Example 4:

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X* (1.8). The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico*. In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (<http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi>) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregius* and *Equus ainus*. *Eumeces egregius* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus* was calculated as 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'ctagtagaatgaatctgaggagg^{3'} and AFR= 5'tatgcaaataggaagtatcattc^{3'}.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa*. These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregius*) for our primers 'mcb398' and 'mcb869', respectively, were higher than the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregius* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

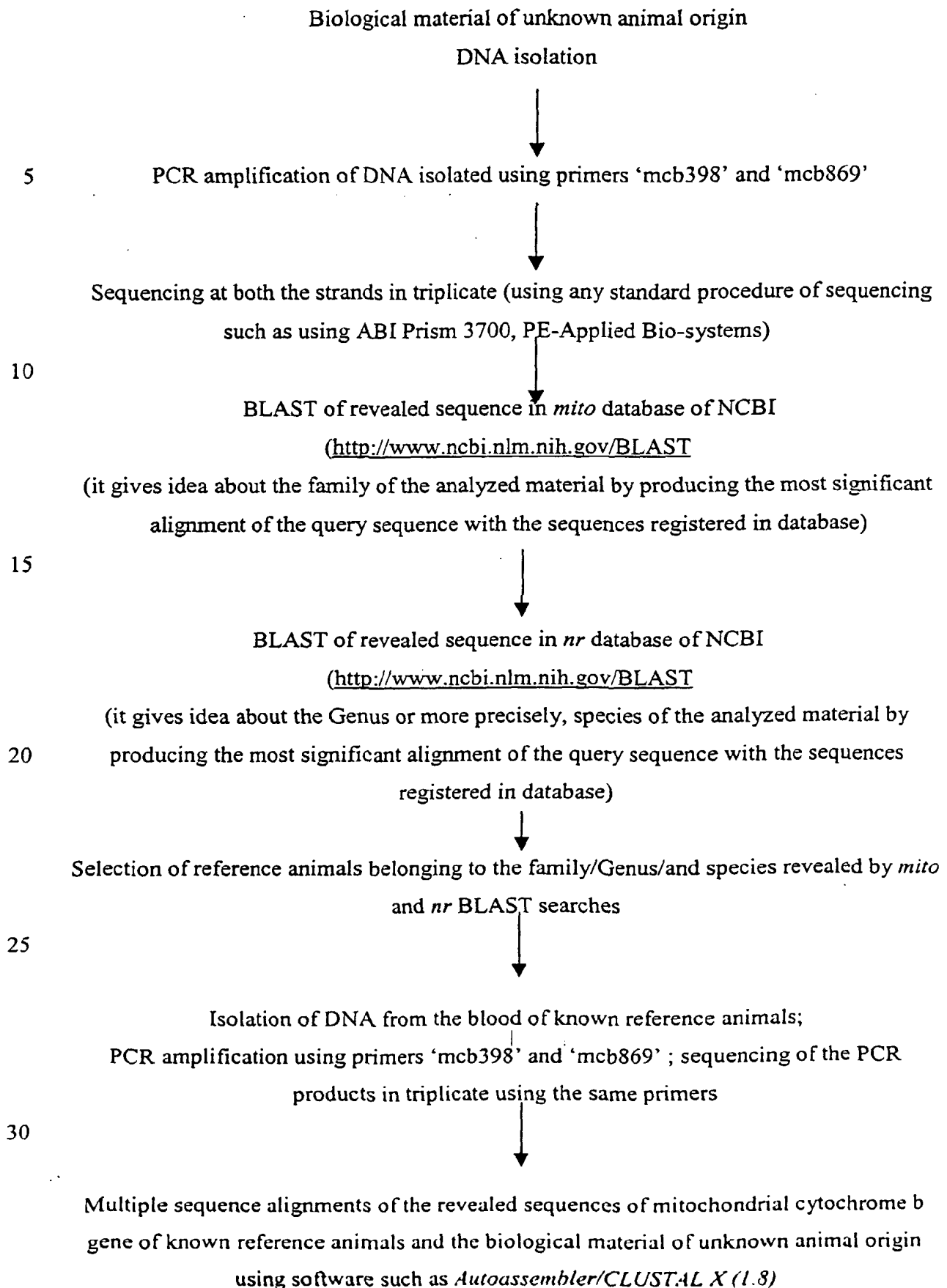
(2) Evidence from bench work/experiments done in laboratory conditions:

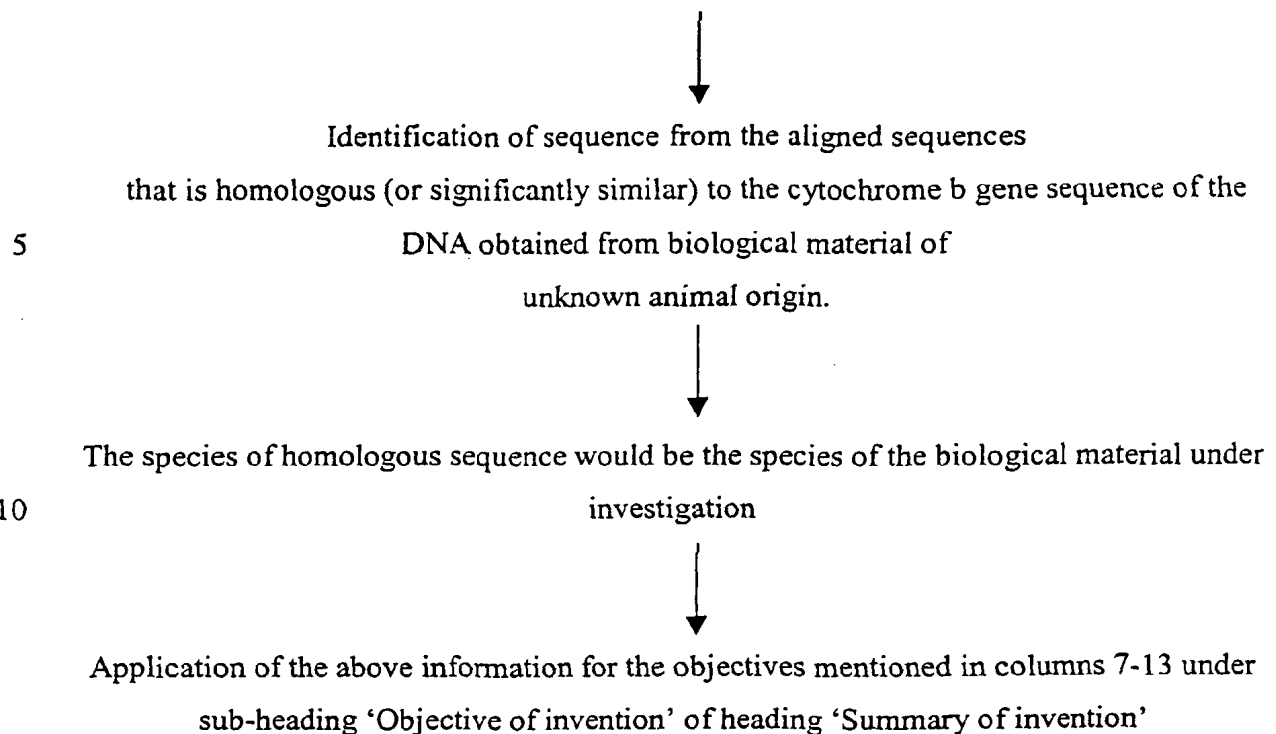
The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869'. The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-wise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:



**Example 6:**

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods⁷⁴ and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 µl reaction volume containing 20 ng of template DNA, 100µm each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of *AmpliTaq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program⁷³. The most significant alignment (bits Value 365, E value e^{-101}) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e^{-170}) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-wise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz11' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a *Panthera pardus* origin. We also calculated the similarity matrix showing the pair-wise similarity amongst the animal species under investigation using *PHYLIP* software. This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source (99.7%, and 98.2 with 'gz11' and 'gz21', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Panthera pardus*) species. The step-wise procedure involved in above analysis is illustrated in Figure 1a, 1b and 1c, respectively.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software⁷³, it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It

5 is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have

identified a fragment on the mitochondrial cytochrome b gene, which has enormous
10 information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer

that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species

15 and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN. Code	Name	NCBI accession #	*P,S/F	*P,S/R
1 aep.mel	<i>Aepyceros melampus</i>	AF036289 ¹	97, 60	94, 62
2 ore.ore	<i>Oreotragus oreotragus</i>	AF036288 ¹	88, 52	94, 62
3 add.nas	<i>Addax nasomaculatus</i>	AF034722 ²	97, 60	95, 66
4 ory.dam	<i>Oryx damah</i>	AJ222685 ¹	90, 58	95, 66
5 hip.equ	<i>Hippotragus equinus</i>	AF022060 ³	98, 63	85, 55
6 alc.bus	<i>Alcelaphus buselaphus</i>	AJ222681 ¹	97, 60	98, 68
7 sig.lic	<i>Sigmoceros lichtensteinii</i>	AF034967 ⁴	97, 60	98, 68
8 bea.hun	<i>Beatragus hunteri</i>	AF034968 ⁴	97, 60	94, 62
9 dam.lun	<i>Damaliscus lunatus</i>	AF016635 ³	97, 60	77, 55
10 con.tau	<i>Connochaetes taurinus</i>	AF016638 ³	82, 56	93, 62
11 bis.bon	<i>Bison bonasus</i>	Y15005 ⁵	90, 58	87, 63
12 bos.gru	<i>Bos grunniens</i> *	AF091631 ⁶	90, 58	94, 62
13 bos.tra	<i>Bos tragocamelus</i> *	AJ222679 ¹	90, 58	95, 66
14 buba.bub	<i>Bubalus bubalis</i> *	D34637 ⁷	97, 60	93, 64
15 bub.min	<i>Bubalus mindorensis</i>	D82895 ⁸	97, 60	87, 62
16 tra.ang	<i>Tragelaphus angasii</i>	AF091633 ⁶	97, 60	87, 63
17 tra.eur	<i>Tragelaphus eurycerus</i>	AF036276 ¹	90, 58	97, 64
18 nem.cau	<i>Nemorhaedus caudatus</i> *	U17861 ⁹	95, 61	93, 59
19 pse.nay	<i>Pseudois nayaaur</i>	AF034732 ²	89, 55	89, 59
20 amm.ler	<i>Ammotragus lervia</i>	AF034731 ²	94, 58	97, 63
21 cap.fal	<i>Capra falconeri</i> *	D84202 ¹⁰	98, 63	95, 66
22 cap.ibe	<i>Capra ibex</i> *	AF034735 ²	98, 63	89, 58
23 hem.jem	<i>Hemitragus jemlahicus</i> *	AF034733 ²	95, 61	90, 61
24 rup.pyr	<i>Rupicapra pyrenaica</i>	AF034726 ²	95, 61	89, 59
25 rup.rup	<i>Rupicapra rupicapra</i>	AF034725 ²	95, 61	94, 64
26 pan.hod	<i>Pantholops hodgsoni</i>	AF034724 ²	98, 63	95, 66
27 bud.tax.tax	<i>Budorcas taxicolor taxicolor</i> *	U17868 ⁹	90, 58	95, 66
28 ovi.amm	<i>Ovis ammon</i> *	AF034727 ²	98, 63	97, 64
29 ovi.vig	<i>Ovis vignei</i> *	AF034729 ²	98, 63	97, 64
30 cap.cri	<i>Capreornis crispus</i> *	AJ304502 ¹¹	98, 63	94, 63
31 ovi.mos	<i>Ovibos moschatus</i>	U17862 ⁹	98, 63	92, 61
32 ore.ame	<i>Oreamnos americanus</i>	AF190632 ¹²	98, 63	94, 62
33 cep.dor	<i>Cephalophus dorsalis</i>	AF091634 ⁶	97, 58	90, 61
34 cep.max	<i>Cephalophus maxwellii</i>	AF096629 ¹³	97, 60	88, 53
35 alc.alc	<i>Alces alces</i>	AJ000026 ¹⁴	95, 61	93, 59
36 hyd.ine	<i>Hydropotes inermis</i>	AJ000023 ¹⁴	97, 60	90, 63
37 mun.mun	<i>Muntiacus muntjak</i> *	AF042713 ¹⁵	90, 58	93, 64
38 cer.ele.kan	<i>Cervus elaphus kansuensis</i> *	AB021098 ¹⁶	98, 63	82, 59
39 cer.ele.xan	<i>Cervus elaphus xanthopygus</i> *	AB021097 ¹⁶	98, 63	82, 59
40 cer.ele.can	<i>Cervus elaphus canadensis</i> *	AB021096 ¹⁶	98, 63	90, 61
41 cer.nip.ce	<i>Cervus nippon centralis</i>	AB021094 ¹⁶	98, 63	90, 61
42 cer.nip.ye	<i>Cervus nippon yessoensis</i>	AB021095 ¹⁶	98, 63	90, 61
43 cer.nip.ke	<i>Cervus nippon keramuc</i>	AB021091 ¹⁶	98, 63	90, 61

44	cer.nip.pu	<i>Cervus nippon pulchellus</i>	AB021090 ¹⁶	98, 63	90, 61
45	cer.nip.ni	<i>Cervus nippon nippon</i>	AB021093 ¹⁶	98, 63	90, 61
46	cer.ela.sc	<i>Cervus elaphus scoticus</i>	AB021099 ¹⁶	98, 63	90, 61
47	cer.dam	<i>Cervus dama</i>	AJ000022 ¹⁴	98, 63	88, 53
48	ran.tar	<i>Rangifer tarandus</i>	AJ000029 ¹⁴	98, 63	89, 57
49	mos.fus	<i>Moschus fuscus</i> *	AF026838 ¹⁷	90, 59	90, 61
50	mos.leu	<i>Moschus leucogaster</i> *	AF026839 ¹⁷	90, 59	90, 61
51	mos.chr	<i>Moschus chrysogaster</i> *	AF026837 ¹⁷	90, 59	90, 61
52	mos.ber	<i>Moschus berezovskii</i> *	AF026836 ¹⁷	90, 59	90, 61
53	mos.mos	<i>Moschus moschiferus</i> *	AF026833 ¹⁷	90, 59	92, 61
54	kob.ell	<i>Kobus ellipsiprymnus</i>	AF022059 ³	91, 61	95, 66
55	kob.meg	<i>Kobus megaceros</i>	AJ222686 ¹	91, 61	83, 56
56	red.aru	<i>Redunca arundinum</i>	AF096623 ¹³	91, 61	94, 62
57	red.ful	<i>Redunca fulvorufula</i>	AF036284 ¹	89, 57	94, 62
58	neo.mos	<i>Neotragus moschatus</i>	AJ222683 ¹	89, 57	94, 62
59	pel.cap	<i>Pelea capreolus</i>	AF022055 ³	91, 61	90, 61
60	ant.cer	<i>Antilope cervicapra</i> *	AF022058 ³	82, 56	93, 64
61	sai.tat	<i>Saiga tatarica</i>	AF064487 ¹⁸	91, 61	92, 61
62	gaz.dam	<i>Gazella dama</i>	AF025954 ³	91, 61	92, 61
63	our.our	<i>Ourebia ourebi</i>	AF036288 ¹	82, 56	82, 59
64	gaz.gaz	<i>Gazella gazella</i> *	AJ222682 ¹	91, 61	89, 57
65	rap.mel	<i>Raphicerus melanotis</i>	AF022053 ³	81, 54	80, 50
66	mad.kir	<i>Madoqua kirkii</i>	AF022070 ³	90, 58	97, 65
67	ant.lame	<i>Antilocapra americana</i>	AF091629 ⁶	98, 63	98, 68
68	tra.jav	<i>Tragulus javanicus</i> *	D32189 ¹⁹	86, 57	86, 59
69	tra.nap	<i>Tragulus napu</i> *	X56288 ²⁰	81, 52	93, 58
70	bal.acu	<i>Balaenoptera acutorostrata</i>	X75753 ²¹	89, 56	97, 61
71	bal.bon	<i>Balaenoptera bonaerensis</i>	X75581 ²¹	89, 56	93, 59
72	bal.bor	<i>Balaenoptera borealis</i> *	X75582 ²¹	89, 56	93, 59
73	bal.edi	<i>Balaenoptera edeni</i>	X75583 ²¹	89, 56	88, 54
74	esc.rob	<i>Eschrichtius robustus</i> *	X75585 ²¹	97, 61	86, 57
75	bal.mus	<i>Balaenoptera musculus</i> *	NC_001601 ²²	97, 57	93, 59
76	meg.nov	<i>Megaptera novaeangliae</i> *	X75584 ²¹	97, 61	94, 63
77	bal.phy	<i>Balaenoptera physalus</i> *	NC_001321 ²³	97, 57	94, 63
78	cap.mar	<i>Caperea marginata</i>	X75586 ²¹	93, 55	91, 53
79	cep.com	<i>Cephalorhynchus commersonii</i>	AF084073 ²⁴	85, 51	88, 55
80	cep.eut	<i>Cephalorhynchus eutropia</i> *	AF084072 ²⁴	85, 51	92, 59
81	lag.obl	<i>Lagenorhynchus obliquidens</i>	AF084067 ²⁴	94, 59	92, 59
82	cep.hez	<i>Cephalorhynchus heavisidii</i>	AF084070 ²⁴	89, 56	97, 63
83	cep.hec	<i>cephalorhynchus hectori</i> *	AF084071 ²⁴	89, 56	92, 59
84	lag.aus	<i>Lagenorhynchus australis</i>	AF084069 ²⁴	86, 54	92, 59
85	lag.cru	<i>Lagenorhynchus cruciger</i>	AF084068 ²⁴	86, 54	92, 59
86	lag.obs	<i>Lagenorhynchus obscurus</i>	AF084066 ²⁴	86, 54	92, 59
87	lis.bor	<i>Lissodelphis borealis</i>	AF084064 ²⁴	85, 51	92, 59
88	lis.per	<i>Lissodelphis peronii</i>	AF084065 ²⁴	86, 54	92, 59
89	glo.mac	<i>Globicephala macrorhynchus</i>	AF084055 ²⁴	94, 59	88, 55
90	glo.mel	<i>Globicephala melas</i>	AF084056 ²⁴	94, 59	88, 55
91	fer.att	<i>Feresa attenuata</i> *	AF084052 ²⁴	94, 59	92, 59

92	pep.ele	<i>Peponocephala electra</i> *	AF084053 ²⁴	94, 59	88, 55
93	gra.gri	<i>Grampus griseus</i>	AF084059 ²⁴	97, 61	89, 59
94	pse.cra	<i>Pseudorca crassidens</i> *	AF084057 ²⁴	94, 59	92, 59
95	lag.acu	<i>Lagenorhynchus acutus</i>	AF084075 ²⁴	98, 63	89, 59
96	orci.bre	<i>Orcinus orca</i>	AF084061 ²⁴	86, 57	82, 52
97	orca.bre	<i>Orcaella brevirostris</i>	AF084063 ²⁴	86, 57	91, 54
98	del.cap	<i>Delphinus capensis</i>	AF084087 ²⁴	96, 54	97, 63
99	del.tro	<i>Delphinus tropicalis</i>	AF084088 ²⁴	97, 57	97, 63
100	del.del	<i>Delphinus delphis</i>	AF084085 ²⁴	97, 57	97, 63
101	sten.cly	<i>Stenella clymene</i>	AF084083 ²⁴	97, 57	97, 63
102	sten.coe	<i>Stenella coeruleoalba</i>	AF084082 ²⁴	97, 57	97, 66
103	tur.adu	<i>Tursiops aduncus</i>	AF084092 ²⁴	97, 57	97, 63
104	sten.fro	<i>Stenella frontalis</i>	AF084090 ²⁴	97, 57	97, 63
105	saus.chi	<i>Sousa chinensis</i>	AF084080 ²⁴	97, 57	88, 59
106	sten.lon	<i>Stenella longirostris</i>	AF084103 ²⁴	97, 61	97, 63
107	turs.tru	<i>Tursiops truncatus</i>	AF084095 ²⁴	97, 57	96, 59
108	lage.alb	<i>Lagenorhynchus alborostris</i>	AF084074 ²⁴	97, 61	97, 66
109	sten.bre	<i>Steno bredanensis</i>	AF084077 ²⁴	97, 61	94, 64
110	sota.flu	<i>Sotalia fluviatilis</i>	AF304067 ²⁵	97, 61	97, 63
111	del.leu	<i>Delphinapterus leucas</i>	U72037 ²⁶	97, 61	95, 66
112	mono.mon	<i>Monodon monoceros</i>	U72038 ²⁶	97, 61	95, 66
113	plat.gan	<i>Platanista gangetica</i> *	AF304070 ²⁵	97, 61	86, 59
114	plat.min	<i>Platanista minor</i> *	X92543 ²⁷	97, 61	86, 59
115	kogi.bre	<i>Kogia breviceps</i>	U72040 ²⁶	97, 59	90, 63
116	kogi.sim	<i>Kogia simus</i>	AF304072 ²⁵	96, 55	92, 63
117	phys.cat	<i>Physeter catodon</i>	AF304073 ²⁵	97, 57	80, 58
118	lipo.vex	<i>Lipotes vexillifer</i> *	AF304071 ²⁵	89, 56	88, 53
119	phoc.sin	<i>phocoena sinus</i>	AF084051 ²⁴	87, 49	92, 62
120	bera.bai	<i>Berardius bairdii</i>	X92541 ²⁷	96, 55	90, 59
121	ziph.car	<i>Ziphius cavirostris</i>	X92540 ²⁷	97, 61	89, 57
122	meso.eur	<i>Mesoplodon europaeus</i>	X92537 ²⁷	97, 57	90, 61
123	meso.bid	<i>Mesoplodon bidens</i>	X92538 ²⁷	97, 61	92, 61
124	meso.den	<i>Mesoplodon densirostris</i>	X92536 ²⁷	91, 61	94, 63
125	hype.amp	<i>Hyperoodon ampullatus</i> *	X92539 ²⁷	97, 61	90, 65
126	meso.per	<i>Mesoplodon peruvianus</i>	AF304074 ²⁵	97, 61	86, 58
127	pont.bla	<i>Pontoparia blainvillei</i>	AF304069 ²⁵	92, 59	88, 55
128	hipp.amp	<i>Hippopotamus amphibius</i>	Y08813 ²⁹	92, 58	95, 66
129	hex.lib	<i>Hexaprotodon liberiensis</i>	Y08814 ²⁹	98, 63	97, 66
130	rhin.son	<i>Rhinoceros sondaicus</i> *	AJ245723 ¹⁰	90, 59	87, 61
131	cera	<i>Ceratotherium simum</i>	NC_001808 ¹²	90, 59	90, 63
132	dic.sum	<i>Dicerorhinus sumatrensis</i>	AJ245723 ¹⁰	90, 59	86, 57
133	equu	<i>Equus asinus</i>	NC_001755 ¹¹	91, 61	73, 51
134	baby.bab	<i>Babyrousa babyrussa</i>	Z50106 ¹¹	89, 56	85, 56
135	phac.af	<i>Phacochoerus africanus</i>	Z50090 ¹¹	90, 59	87, 54
136	sus.scr.ew	<i>Sus scrofa haplotype EWBJ</i> *	AF136549 ¹⁴	97, 57	83, 54
137	sus.bar	<i>Sus barbatus</i>	Z50107 ¹¹	97, 57	85, 55
138	lama.gla	<i>Lama glama</i>	U06429 ¹¹	89, 55	85, 53
139	lama.gua	<i>Lama guanicoe</i>	Y08812 ²⁹	88, 54	86, 57

140 vic.vic	<i>Vicugna vicugna</i>	U06430 ³⁵	89, 55	85, 53
141 cam.bac	<i>Camelus bactrianus</i>	U06427 ³⁵	94, 58	86, 58
142 arc.for	<i>Arctocephalus forsteri</i>	X82293 ³⁶	97, 60	87, 64
143 arc.gaz	<i>Arctocephalus gazella</i>	X82292 ³⁶	94, 58	87, 64
144 eum.jub	<i>Eumetopias jubatus</i>	X82311 ³⁶	97, 57	86, 57
145 zal.cal	<i>Zalophus californianus</i>	X82310 ³⁶	89, 55	86, 57
146 odo.ros	<i>Odobenus rosmarus</i>	X82299 ³⁶	91, 61	81, 52
147 pho.vit	<i>Phoca vitulina</i>	X82306 ³⁶	90, 58	87, 64
148 pho.fascia	<i>Phoca fasciata</i>	X82302 ³⁶	98, 63	95, 66
149 pho.gro	<i>Phoca groenlandica</i>	X82303 ³⁶	92, 59	90, 61
150 cys.cri	<i>Cystophora cristata</i>	X82294 ³⁶	89, 56	87, 64
151 hyd.lep	<i>Hydrurga leptonyx</i>	X82297 ³⁶	89, 55	82, 54
152 lep.wed	<i>Leptonychotes weddelli</i>	X72005 ³⁷	98, 63	91, 66
153 mir.leo	<i>Mirounga leonina</i>	X82298 ³⁶	89, 55	82, 59
154 eri.bar	<i>Erignathus barbatus</i>	X82295 ³⁶	89, 56	87, 63
155 mon.sch	<i>Monachus schauinslandi</i>	X72209 ³⁷	91, 61	87, 60
156 hela.mal	<i>Helarctos malayanus</i> *	U18899 ³⁸	84, 54	90, 63
157 sel.thi	<i>Selenarctos thibetanus</i> *	AB020910 ³⁹	89, 57	87, 64
158 ail.ful	<i>Ailurus fulgens</i> *	X94919 ⁴⁰	93, 55	87, 64
159 fel	<i>Felis catus</i>	NC_001700 ⁴¹	85, 56	90, 63
160 can	<i>Canis familiaris</i>	NC_002008 ⁴²	98, 58	84, 54
161 tal	<i>Talpa europaea</i>	NC_002391 ⁴³	81, 50	92, 57
162 gla.sab	<i>Glaucomys sabrinus</i>	AF011738 ⁴⁴	90, 59	82, 54
163 gla.vol	<i>Glaucomys volans</i>	AB030261 ⁴⁵	90, 59	87, 60
164 hyl.pha	<i>Hylomys phayrei</i> *	AB030259 ⁴⁵	91, 61	81, 50
165 pet.set	<i>Petinomys setosus</i> *	AB030260 ⁴⁵	91, 61	81, 50
166 bel.pea	<i>Belomys pearsonii</i> *	AB030262 ⁴⁵	91, 61	87, 64
167 pte.mom	<i>Pteromys momonga</i> *	AB030263 ⁴⁵	97, 61	90, 63
168 gala.demi	<i>Galagoides demidoff</i>	AF271411 ⁴⁶	97, 58	87, 64
169 pero.pot	<i>Perodicticus potto</i>	AF271413 ⁴⁶	97, 60	87, 63
170 gala.mat	<i>Galago matschiei</i>	AF271409 ⁴⁶	97, 60	90, 61
171 gala.moh	<i>Galago moholi</i>	AF271410 ⁴⁶	97, 57	95, 66
172 oto.gar	<i>Otolemur garnettii</i>	AF271412 ⁴⁶	92, 58	87, 60
173 lor.tar	<i>Loris tardigradus</i> *	U53581 ⁴⁷	97, 60	93, 59
174 nyc.cou	<i>Nycticebus coucang</i> *	U53580 ⁴⁷	97, 60	95, 66
175 mus	<i>Mus musculus</i>	NC_001569 ⁴⁸	97, 60	86, 59
176 gor	<i>Gorilla gorilla</i>	NC_001645 ⁴⁹	89, 57	80, 58
177 homo	<i>Homo sapiens sapiens</i>	NC_001807 ⁵⁰	96, 55	84, 64
178 dug.dug	<i>Dugong dugong</i> *	U07564 ⁵¹	97, 60	89, 59
179 ele.max	<i>Elephas maximus</i> *	AB002412 ⁵²	97, 60	76, 57
180 afr.con	<i>Afropavo congensis</i>	AF013760 ⁵³	97, 58	87, 63
181 pavo.mut	<i>Pavo muticus</i> *	AF013763 ⁵³	97, 57	87, 63
182 tra.bly	<i>Tragopan blythii</i> *	AF200722 ⁵⁴	89, 55	85, 57
183 tra.sat	<i>Tragopan satyra</i> *	AF229837 ⁵⁴	89, 55	86, 61
184 tra.cob	<i>Tragopan caboti</i>	AF200723 ⁵⁴	89, 55	86, 61
185 tra.tem	<i>Tragopan temminckii</i> *	AF023802 ⁵⁵	89, 55	81, 56
186 arg.arg	<i>Argusianus argus</i>	AF013761 ⁵³	89, 55	87, 63
187 cat.wal	<i>Catrecus wallichi</i> *	AF023792 ⁵³	88, 54	85, 57

188	cro.cro	<i>Crossoptilon crossoptilon</i> *	AF028794 ⁵³	89, 55	85, 57
189	sym.rec	<i>Syrnaticus reevesi</i> *	AF028801 ⁵³	89, 55	85, 57
190	bam.tho	<i>Bambusicola thoracica</i> *	AF028790 ⁵³	80, 48	94, 64
191	fra.fra	<i>Francolinus francolinus</i>	AF013762 ⁵³	97, 58	86, 61
192	ith.cru	<i>Ithaginis cruentus</i> *	AF068193 ⁵³	98, 63	85, 57
193	ant.par	<i>Anthropoides paradisea</i>	U27557 ⁵⁶	85, 56	82, 58
194	ant.vir	<i>Anthropoides virgo</i>	U27545 ⁵⁶	84, 54	82, 52
195	gru.ant.an	<i>Grus antigone antigone</i>	U11060 ⁵⁷	90, 53	87, 63
196	gru.ant.gi	<i>Grus antigone gillae</i>	U11064 ⁵⁷	90, 53	87, 63
197	gru.any.sh	<i>Grus antigone sharpei</i>	U11061 ⁵⁷	90, 53	87, 63
198	gru.leu	<i>Grus leucogeranus</i> *	U27549 ⁵⁶	90, 53	87, 63
199	gru.can.pr	<i>Grus canadensis pratensis</i>	U27553 ⁵⁶	97, 60	87, 63
200	gru.can.ro	<i>Grus canadensis rowani</i>	U27552 ⁵⁶	97, 60	87, 63
201	gru.can.ta	<i>Grus canadensis tabida</i>	U27551 ⁵⁶	98, 63	87, 63
202	gru.can.ca	<i>Grus canadensis canadensis</i>	U27554 ⁵⁶	97, 61	87, 63
203	gru.ame	<i>Grus americana</i>	U27555 ⁵⁶	90, 53	87, 63
204	gru.gru	<i>Grus grus</i>	U27546 ⁵⁶	89, 54	87, 63
205	gru.mon	<i>Grus monacha</i> *	U27548 ⁵⁶	90, 53	87, 63
206	gru.nig	<i>Grus nigricollis</i> *	U27547 ⁵⁶	90, 53	87, 63
207	gru.jap	<i>Grus japonensis</i>	U27550 ⁵⁶	81, 54	87, 63
208	cic.boy	<i>Ciconia boyciana</i> *	NC_002196 ⁵⁸	94, 58	79, 60
209	rhe.ame	<i>Rhea americana</i>	AF090339 ⁵⁹	93, 63	79, 60
210	ant.alb	<i>Anthracoeros albirostris</i> *	U89190 ⁶⁰	97, 61	86, 59
211	fal.fam	<i>Falco femoralis</i>	U83310 ⁶¹	97, 61	86, 60
212	fal.ver	<i>Falco verpertinus</i>	U83311 ⁶¹	97, 61	85, 57
213	fal.par	<i>Falco peregrinus</i> *	U83307 ⁶¹	97, 61	84, 52
214	fal.spa	<i>Falco sparverius</i>	U83306 ⁶¹	92, 59	80, 51
215	ayt.ame	<i>Aythya americana</i>	NC_000877 ⁶²	98, 63	94, 62
216	smi.sha	<i>Smithornis sharpei</i>	NC_000879 ⁵⁹	97, 58	90, 61
217	vid.cha	<i>Vidua chalybeata</i>	NC_000880 ⁵⁹	97, 60	87, 64
218	chry.pic	<i>Chrysemys picta</i>	NC_002073 ⁶³	89, 56	86, 57
219	emy.orb.ku	<i>Emys orbicularis</i>	AJ131425 ⁶⁴	90, 59	94, 63
220	che.mud	<i>Chelonia mydas</i> *	AB012104 ⁶⁵	90, 58	94, 63
221	eum.egr	<i>Eumeces egregius</i>	AB016606 ⁶⁵	86, 55	73, 51

Table 2. Multiple sequence alignment of 471 bp fragment of mitochondrial cytochrome b gene of 221 animal species

PRIMER 'mcb193'	TACCATGAGGACAAATATCATTCTG	
aep.mel	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA	60
ore.ore	TTCCCTGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACTAATCTCCTCTCAGCAA	60
add.nas	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
ory.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACTAACCTCTCTCAGCAA	60
hip.equ	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
alc.bus	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
sig.lic	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
bea.hun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
dam.lun	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCTCTCAGCAA	60
con.tau	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
amm.ler	TGCCATGAGGACAGATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
pse.nay	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
cap.ibe	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
hem.jem	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
cap.fal	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCAA	60
rup.pyt	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCGA	60
rup.rup	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCTCAGCAA	60
nem.cau	TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCTCTCAGCAA	60
bud.tax.tax	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
pan.hod	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.amm	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.vig	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
cap.cri	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCTCTCAGCAA	60
ovi.mos	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAATCTCCTTTTCAAGAA	60
ore.ame	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
cep.dor	TGCCATGAGGAGCAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
cep.max	TGCCATGAGGAGCAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bis.bon	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bos.gru	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCTCTCAGCAA	60
bos.tra	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAATCTATTATCAGCAA	60
bub.min	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
buba.bub	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
tra.ang	TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
tra.eur	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
kob.ell	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
kob.meg	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
red.aru	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
red.ful	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
neo.mos	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
pel.cap	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
gas.dam	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
our.our	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
ant.gar	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
sal.tat	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
mad.kir	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
rap.mel	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
gas.gas	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
ant.ame	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
hyd.ine	TGCCATGAGGACAAATATCCTTTTGAGGAGCAACAGTTATCACCACCTCTCTCAGCAA	60
mun.mun	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
alc.ala	TACCATGAGGACAGATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60
cer.ela.kun	TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCACCTCTCTCAGCAA	60

cer.ela.xan	TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTTCTCTCAGCAA	60
cer.ela.can	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.cent	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.yes	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.ker	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.pul	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.nip.nip	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.ela.sco	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cer.dam	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
ran.tar	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mos.fus	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mos.leu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mos.chr	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mos.ber	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mos.mos	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
tra.jav	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
trag.nap	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.acu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.bon	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.bor	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.edi	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
esch.rob	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.mus	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
mega.nov	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
bala.phy	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
cap.mar	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
ceph.com	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
ceph.euc	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.obl	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
ceph.heu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
ceph.hec	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.aus	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.cru	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.obs	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lisso.bor	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lisso.per	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
glo.mac	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
glo.mel	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
fere.att	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
pepo.ele	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
gram.gri	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
pse.cra	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.acu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
orci.bre	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
orca.bre	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
del.cap	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
del.tro	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
del.del	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sten.cly	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sten.coe	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
tur.adu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sten.fro	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
saus.chi	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sten.lon	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
turs.tru	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
lage.alb	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sten.bre	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60
sota.flu	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA	60

del.leu	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA	60
mono.mon	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA	60
plat.gan	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	60
plat.min	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	60
kogi.bre	TACCCTGAGGACAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATATCCGCAA	60
kogi.sim	TGCCCTGAGGACAAATATCATTCTGAGGAGCAACCGTCATCACAAACCTTATATCCGCAA	60
phys.cat	TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACAAACCTTCTATCAGCAA	60
lipo.vex	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTTCTATCAGCAA	60
phoc.sin	TGCCCTGAGGACAAATATCATTCTGAGGTGCTACCGTCATCACAAACCTCCTATCAGCAA	60
bera.bai	TGCCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCCGCTA	60
ziph.car	TACCTTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACAAACCTCCTATCCGCTA	60
meso.eur	TTCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATTACCAACCTCCTATCCGCCA	60
meso.bid	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCTGTTATTACTAACCTCCTATCCGCTA	60
meso.den	TACCATGAGGACAAATATCCTTCTGAGGTGCAACCTGTCATTACCAATCTTCTATCCGCTA	60
hype.amp	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCCGCCA	60
meso.per	TACCTTGAGGACAAATATCATTCTGAGGCGCAACCTGTCATTACTAATCTTTTATCTGCTA	60
pont.bla	TACCCTGAGGACAAATGTCATTCTGAGGTGCCACTGTCATCACTAACCTCCTATCAGCCA	60
hex.lib	TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACTTACTATCAGCTA	60
hipp.amp	TGCCATGAGGACAAATGTCATTCTGAGGGGCAACAGTCATTACCAACTTACTGTCAGCTA	60
dic.sum	TACCATGAGGTCAAATATCCTTCTGAGGAGGCAAGTTATCACAAATCTCCTCTCAGCCA	60
rhin.son	TACCATGAGGTCAAATATCCTTCTGAGGGGCTACAGTCATTACAAATCTCCTCTCAGCCA	60
cera	TACCATGAGGCCAAATATCCTTCTGAGGGGCTACAGTCATCACAAACCTCCTCTCAGCTA	60
equu	TACCATGAGGACAAATATCCTTCTGAGGAGCAACCGTCATTACAAACCTCCTATCAGCAA	60
baby.bab	TACCTTGAGGACAAATATCATTCTGAGGAGCTACCGTCATTACAAACCTACTATCAGCCA	60
phac.afr	TACCCTGAGGACAAATATCGTTCTGAGGAGCCACAGTCATCACAAACCTACTATCAGCCA	60
sus.bar	TGCCCTGAGGACAAATATCATTCTGAGGAGCTACCGTCATCACAAATCTACTATCAGCTA	60
sus.scr.ewb3	TGCCCTGAGGACAAATATCATTCTGAGGAGCTACCGTCATCACAAATCTACTATCAGCTA	60
lama.gla	TCCCATGAGGACAAATATCATTCTGAGGGGCAACAGTAATTACAAATCTACTCTCGGCCA	60
lama.gua	TCCCATGAGGCCAAATATCATTCTGAGGGGCAACAGTAATTACAAACCTACTCTCGGCCA	60
vic.vic	TCCCATGAGGACAAATATCATTCTGAGGGGCAACAGTAATTACAAACCTACTCTCAGCAA	60
cam.bac	TCCCATGAGGACAGATATCATTCTGAGGAGCAACAGTAATTACAAACCTACTCTCAGCAA	60
arc.for	TTCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG	60
arc.gaz	TTCCATGAGGACAGATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAA	60
eum.jub	TTCCGTGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCTA	60
sal.cal	TTCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG	60
odo.ros	TACCATGAGGACAAATATCCTTCTGAGGAGCAACCGTCATCACCAACCTTCTGTCAGCAA	60
pho.fasciata	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAATCTACTATCAGCAA	60
pho.gro	TACCATGAGGGCAAATGTCATTCTGAGGAGCAACAGTTATCACTAATCTACTATCAGCAA	60
pho.vit	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACTTACTATCAGCAA	60
cys.cri	TACCGTGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACTTACTATCAGCAA	60
hyd.lep	TGCCATGAGGACAAATATCATTCTGAGGAGCAACCGTTATTACCAACTTACTATCAGCAA	60
lep.wed	TACCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACTTACTATCAGCAA	60
mir.leo	TGCCATGAGGACAAATATCATTCTGAGGAGCAACCGTCATTACCAACCTACTATCAGCAG	60
eri.bar	TACCATGAGGGCAAATATCATTCTGAGGAGCAACCGTTATCACCAACCTACTATCAGCAA	60
mon.sch	TACCATGAGGACAAATATCCTTCTGAGGGGCGACCGTCATCACCAACCTACTATCAGCAA	60
hela.mal	TACCCTGAGGCCAAATGTCCTTCTGAGGAGCAACCTGTCATTACCAATCTCCTATCAGCCA	60
sel.thi	TACCCTGAGGCCAAATATCCTTCTGAGGAGCGACTGTCATTACCAACCTCCTATCAGCCA	60
ail.ful	TGCCCTGAGGACAGATATCATTCTGAGGAGCAACCGTTATCACCAACCTACTATCAGCCA	60
fel	TACCATGAGGCCAAATGTCCTTCTGAGGAGCAACCGTAATCACTAAGCTCCTGTCAGCAA	60
can	TACCATGAGGACAAATATCATTCTGAGGAGCAACCTGTAATCACTAATCTTCTCTGCGCA	60
tal	TACCATGGGGTCAAATATCCTTTTGAGGTGCAACCGTAATTACAAATTTACTGTCAGCCA	60
gla.sab	TACCCTGAGGACAAATATCTTTCTGAGGAGCAACCGTCATCACCAACCTTCTCTCAGCTA	60
gla.vol	TACCCTGAGGACAAATATCTTTCTGAGGAGCTATGTCATCACCAACCTTCTCTCAGCTA	60
hyl.pha	TACCATGAGGACAAATATCTTTCTGAGGGGCTACCGTTATTACAAACCTACTATCTGCCA	60
pet.sec	TACCATGAGGACAAATATCTTTCTGAGGGGCTACCGTTATTACAAACCTACTATCTGCCA	60
bel.pea	TACCATGAGGACAAATATCTTTCTGAGGAGCAACCTGTAATCACTAAGCTCCTGTCAGCTA	60
pte.mom	TACCCTGAGGACAAATATCATTCTGAGGGGCGACTGTCATCACCAACCTCCTATCCGCCA	60
gala.demi	TTCCATGAGGCCAAATATCATTCTGAGGTGCTA TGGTAATCACTAAGCTCCTGTCAGCTA	60

pero.pot	TCCCATGAGGACAAATATCATTTCTGAGGTTGCCACAGTAATCACAACCTCCTATCAGCAA	60
gala.mat	TCCCATGAGGACAAATATCATTTCTGAGGCGCTACCGTAATCACAATCTCCTCTCGCAA	60
gala.moh	TTCCGTGAGGACAAATATCATTTCTGAGGCGCTACCGTAATCAGTAACCTCCTCTCAGCAA	60
oto.gar	TCCCATGAGGACAAATGTCTATTTCTGAGGCGCAACCGTAATTACAAATCTCCTCTCAGCAA	60
lor.tar	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACAGTAATTACCAACCTACTATCAGCAA	60
nyc.cou	TCCCATGAGGACAAATATCATTTCTGAGGTTGCCACCGTCATCACTAACCTACTATCGGCAA	60
mus	TTCCATGAGGACAAATATCATTTCTGAGGTTGCCACAGTTATTACAAACCTCCTATCAGCAA	60
gorr	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACAGTAATCACAACCTTGTCTATCGGCAA	60
homo	TCCCGTGAGGACAAATATCATTTCTGAGGAGCCACAGTAATCACAACCTTACTATCGGCAA	60
dug.dug	TCCCATGAGGACAAATATCATTTCTGAGGAGCAACCGTTATTACTAACCTCCTCTCAGCTA	60
ele.max	TTCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
afr.con	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
pavo.mut	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
tra.bly	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
tra.sat	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
tra.cob	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
tra.tem	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
arg.arg	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
cat.wal	TTCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
cro.cro	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
sym.ree	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
bam.tho	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
fra.fra	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
ith.cru	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
ant.par	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
ant.vir	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.ant.ant	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.ant.gil	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.ant.sha	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.leu	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.can.pra	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.can.row	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.can.tab	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.can.can	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.ame	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.gru	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.mon	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.nig	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
gru.jap	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
cic.boy	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
rhe.ame	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
ant.alb	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
fal.fam	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
fal.ver	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
fal.per	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
fal.spa	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
ayt.ame	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
smi.sha	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
vid.cha	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
chry.pic	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
emy.orb.kur	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
che.mud	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
eum.egr	TCCCATGAGGACAAATATCATTTCTGAGGAGCCACCGTAATTACTAACCTCCTCTCAGCAA	60
...
sep.mel	TCCCATATATTGCCACAAACCTAGTACAATGAATCTTGAAGAGGATTTCTCTCTAGCAAAG	120
ora.ora	TCCCATATATTGCCACAAACCTAGTACAATGAATCTTGAAGAGGATTTCTCTCTAGCAAAG	120
add.nas	TCCCATATATTGCCACAAACCTAGTACAATGAATCTTGAAGAGGATTTCTCTCTAGCAAAG	120

ory.dam	TCCCATACATCGGCACAAATCTAGTCGAATGAATTTGAGGGGGATTCTCCGTAGACAAAG	120
hip.equ	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCCGTAGACAAAG	120
alc.bus	TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
sig.lic	TCCCATATATTGGGCACAGACCTAGTAGAATGAATCTGAGGAGGATTATCAGTAGACAAAG	120
bea.hun	TTCCATATATTGGTACAAACCTAGTCGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAG	120
dam.lun	TTCCATACATCGGCACAAATCTAGTCGAATGGATCTGAGGGGGCTTCTCAGTAGACAAAG	120
con.tau	TCCCATACATTGGGCACTAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
amm.les	TCCCATACATTGGGCACAGACCTGGTTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
psa.nay	TCCCCTATATTGGGCACAAATCTAGTCGAATGGATCTGAGGGGGATTCTCAGTAGACAAAG	120
cap.ibe	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
hem.jem	TTCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTAGACAAAG	120
cap.fal	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTAGATAAAG	120
rup.pyr	TCCCATACATTGGGCATAGACTTAGTCGAGTGAATCTGAGGGGGCTTCTCCGTAGACAAAG	120
rup.rup	TCCCCTATATTGGGCACAGACTTAGTCGAATGAATCTGAGGAGGCTTCTCCGTAGACAAAG	120
nem.cau	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
bud.tax.tax	TCCCATACATTGGGCACAAACCTAGTTGAGTGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
pan.hod	TCCCATACATTGGGCACAGACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
ovi.amm	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
ovi.vig	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTAGACAAAG	120
cap.cri	TCCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCCGTAGACAAAG	120
ovi.mos	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCCGTAGACAAAG	120
ore.ame	TTCCATACATCGGTACAGACCTAGTCGAATGAATCTGAGGGGGGTTCTCAGTAGACAAAG	120
cap.dor	TCCCATACATTGGTACAAACCTAGTCGAATGAATCTGAGGAGGCTTTTTCAGTAGACAAAG	120
cap.max	TCCCATATATCGGCACAAACCTAGTTGAGTGAATCTGAGGGGGCTTTTTCAGTAGACAAAG	120
bis.bon	TCCCATACATCGGCACAAATCTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG	120
bos.gru	TTCCATACATCGGCACAAATTTAGTCGAATGGATTGAGGTGGGTTCTCAGTAGACAAAG	120
bos.tre	TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGCGGTTCTCAGTAGACAAAG	120
bub.min	TCCCATACATTGGGCACAAACCTAGTTGAGTGAATTTGAGGGGGATTCTCAGTAGACAAAG	120
buba.bub	TCCCATACATTGGTACAAAGCTGGTTGAATGAATTTGAGGGGGATTCTCAGTAGACAAAG	120
tra.ang	TCCCATATATTGGGCACCAACCTAGTTGAATGAATCTGAGGAGGCTTCTCCGTAGACAAAG	120
tra.eur	TCCCCTATATTGGGCACCGACCTAGTCGAATGAATCTGAGGGGGCTTTTTCAGTAGACAAAG	120
kob.eil	TTCCATACATTGGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTAGATAAGG	120
kob.meg	TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTAGACAAAG	120
red.aru	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTCGATAAAG	120
red.ful	TCCCATACATCGGCACAAACCTAGTTGAATGAATCTGAGGAGGTTCTCAGTCGATAAAG	120
rac.mos	TCCCATATATCGGCACAAACCTAGTCGAATGAATCTGAGGGGGCTTCTCAGTAGACAAAG	120
pel.cap	TCCCATACATTGGTACAAACCTAGTCGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
gas.dam	TCCCATACATCGGCACAAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTAGATAAGG	120
our.our	TTCCATACATTGGTACAAACCTAGTCGAATGAATCTGAGGAGGTTCTCAGTAGACAAAG	120
ant.cer	TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG	120
sai.tac	TCCCATATATCGGCACAGACCTAGTAGAATGAATCTGAGGGGGTTTTTTCAGTAGATAAAG	120
mad.kir	TCCCATATATCGGCACAAACCTAGTTGAATGAATCTGAGGGGGCTTCTCAGTAGACAAAG	120
rap.mel	TTCCCTACATTGGGCACAAACCTAGTAGAATGGATCTGAGGAGGATTCTCAGTTGATAAAG	120
gas.gas	TCCCATACATCGGCACAAACCTAGTAGAATGAATCTGAGGGGGATTCTCCGTAGATAAAG	120
ant.ame	TCCCATACATTGGTACTAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAG	120
hyd.ine	TTCCATACCTCGGTACAAATCTAGTCGAATGAATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
mun.mun	TTCCATATATTGGGCACAAACCTAGTCGAATGAATCTGAGGAGGCTTTTTCAGTTGATAAAG	120
alc.alc	TTCCATACATTGGTACTAATCTAGTTGAATGAATTTGAGGGGGTTTTTTCAGTAGACAAAG	120
cer.ela.kan	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.ela.kan	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.ela.gin	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.nip.cen	TTCCATATATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.nip.yes	TTCCATATATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.nip.ker	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.nip.pul	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.nip.nip	TTCCATACATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGATAAAG	120
cer.ela.gin	TTCCATATATTGGGCACAAACCTAGTCGAATGGATCTGAGGAGGCTTTTTCAGTAGACAAAG	120
cer.dam	TCCCATACATTGGTACAAACCTAGTTGAATGAATCTGAGGGGGTTTTTTCAGTAGACAAAG	120

ran. car	TTCCATATATTGGTACAAATCTAGTGGAAATGAATTTGAGGAGGATTTTCTGTAGATAAAG	120
mos. fus	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos. leu	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos. chr	TTCCATACATTGGTACTAAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos. ber	TTCCCTACATTGGTACTAAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
mos. mos	TTCCCTACATTGGTACTAAATCTGGTTGAATGAATTTGAGGAGGCTTCTCAGTAGACAAAG	120
tra. jav	TCCCATACATTGGGACAGAGCTTGGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
trag. nap	TCCCTATATTCGGCACCGAATAGTTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. acu	TCCCATATATTGGTACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. bon	TCCCATACATTGGTACCACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. bor	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. edi	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
esch. rob	TCCCATACATTGGGACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. mus	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
mega. nov	TCCCATACATTGGTACTACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
bala. phy	TCCCATACATTGGTACCACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
cap. mar	TCCCATATATTGGTACCACCTTAGTGAATGAATCTGAGGCGGCTTCTCAGTAGACAAAG	120
ceph. com	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph. eut	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage. obl	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph. hea	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
ceph. hec	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage. aus	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage. cru	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lage. obs	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso. bor	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
lisso. per	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG	120
glo. mac	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
glo. mel	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
fere. att	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
pepo. ele	TCCCTACATCGGAACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
gram. gri	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
pse. cra	TCCCTACATCGGTACTACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
lage. acu	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
orci. bre	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
orca. bre	TCCCTACATCGGCACCACCTTAGTAGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
del. cap	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
del. tro	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
del. del	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sten. cly	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sten. coe	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
tur. adu	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sten. fro	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
saus. chi	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sten. lon	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
turs. tru	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
lage. alb	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sten. bre	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
sota. flu	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
del. leu	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
mono. mon	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
plat. gan	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
plat. min	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
kogi. bre	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
kogi. sim	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
phys. cut	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
lipo. wak	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120
phoc. sin	TCCCTATATTGGGCACTACCTTAGTGAATGAATCTGAGGTGGAATTTCCGTAGACAAAG	120

bera.bai	TTCCCTTATATCGGCACCACTCTTGTGGAATGAATCTGAGGTGGCTTTCTCCGTAGATAAAAG	120
ziph.car	TCCCTTATATCGGCACCTACTCTAGTGAATGAATCTGAGGTGGCTTTCTCCGTAGATAAAAG	120
meso.eur	TCCCTTATATCGGCACCTACTCTAGTGAATGAATCTGAGGTGGCTTTCTCCGTAGATAAAAG	120
meso.bid	TTCCCTACATCGGCACCTACCCTAGTGAATGAATCTGAGGTGGCTTTCTCCGTAGACAAAAG	120
meso.den	TTCCCTTATATCGGCACCACTACTAGTGAATGAATCTGAGGTGGCTTTCTCCGTAGACAAAAG	120
hype.amp	TTCCCTTATATCGGCACCTACCCTAGTGAATGAATCTGAGGTGGCTTTCTCCGTAGACAAAAG	120
meso.per	TCCCTTATATTTGGCACCACCTAGTGAATGAATTTGAGGTGGCTTTCTCCGTAGATAAAAG	120
pons.bla	TCCCTTACATCGGAACCTACCCTTGTAGAATGGATCTGAGGTGGCTTTCTCTGTAGACAAAAG	120
hex.lib	TCCCTTACATTTGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTCTCTGTAGATAAAAG	120
hipp.amp	TCCCTTATATTTGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTCTCCGTAGACAAAAG	120
dic.sum	TCCCATACATCGGCACCGACCTTGTAGAATGAATCTGAGGGGGATTTCTCCGTAGACAAAAG	120
rhin.son	TCCCTTATATCGGTACCAACCTTGTAGAGTGAATCTGAGGAGGATTCTCAGTCGACAAAAG	120
cera	TCCCTTACATCGGCACCAACCTCGTAGAATGAATCTGAGGTGGATTCTCAGTAGACAAAAG	120
equu	TCCCTTACATCGGTACTACCTCGTGAATGAATCTGAGGTGGATTCTCAGTAGACAAAAG	120
baby.bab	TTCCCTTATATCGGAACCGACCTCGTAGAATGGATCTGAGGAGGCTTTCTCCGTGACAAAAG	120
phac.afr	TCCCTTACATTTGGAACCAATCTTGTAGAATGAATCTGAGGAGGTTTCTCCGTGACAAAAG	120
sus.bar	TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTCTCCGTGACAAAAG	120
sus.scr.ewb3	TCCCTTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTCTCCGTGACAAAAG	120
lama.gla	TTCCATATGTTGGCACAACACTAGTGAATGAATTTGAGGAGGATTCTCCGTAGACAAAAG	120
lama.gua	TTCCATATGTTGGCACAACACTAGTGAATGAATTTGAGGGGGGTTCTCCGTAGATAAAAG	120
vic.vic	TTCCATACGTTGGTACAACACTAGTGAATGAATTTGAGGAGGATTCTCCGTAGATAAAAG	120
cam.bac	TTCCCTTATATCGGCACCAACCTAGTAGAATGAATTTGAGGTGGCTTTCTCCGTAGACAAAAG	120
arc.for	TCCCTTACATTTGGGACCAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
arc.gaz	TCCCTTACATCGGAACCTAACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
eum.jub	TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTCGACAAAAG	120
zal.cal	TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTCTCAGTCGACAAAAG	120
odo.ros	TTCCCTATGTTAGGGAGCTGACTTGGTGAATGAGTCTGAGGGGGGTTTCTCAGTTGATAAAG	120
pho.fasciata	TTCCCTTATATCGGAACCGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGATAAAG	120
pho.gro	TCCCTTACATCGGAACCGATCTAGTAGAATGAATCTGAGGAGGTTCTCAGTTGATAAAG	120
pho.vit	TCCCTTATGTTGGGAACCGACCTTGTAGAATGAATCTGAGGAGGTTTCTCAGTAGATAAAG	120
cys.cri	TCCCTTACATCGGAGCCGATCTAGTAGAATGAATCTGAGGGGGATTCTCAGTCGATAAAG	120
hyd.lep	TTCCCTTACATCGGAACCGACCTAGTAGAATGAATTTGAGGCGGATTCTCAGTCGACAAAAG	120
lep.wed	TTCCCTTACATCGGAACCTGACTTAGTAGAATGAATCTGAGGCGGATTCTCAGTTGACAAAAG	120
mir.leo	TCCCTTATGTTGGGAGACGACCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
eri.bar	TCCCTTACATCGGACCTGATCTAGTAGAATGAATCTGAGGAGGATTCTCAGTTGACAAAAG	120
mon.sch	TCCCTTACATCGGAACCGATCTAGTAGAATGAATCTGAGGCGGTTCTCAGTAGATAAAG	120
hela.mal	TCCCTTATATTTGGAACCGACCTAGTAGAATGAATCTGAGGAGGCTTTCTCCGTAGACAAAG	120
sel.thi	TCCCTTATATTTGGAACAGACCTAGTAGAATGAATCTGAGGGGGCTTTCTCTGTAGATAAAG	120
ail.ful	TTCCCTTATATTTGGAACCTAACCTTGTAGAGTGAATCTGAGGAGGTTTCTCAGTCGACAAAAG	120
fel	TTCCATACATCGGCACTGAACCTAGTAGAATGAATCTGAGGGGGGTTCTCAGTAGACAAAAG	120
can	TCCCTTATATCGGCACTGACTTAGTAGAATGGATCTGAGGCGGCTTCTCAGTGGACAAAAG	120
tal	TTCCCTTACATCGGTACAGACTTAGTAGAATGAATTTGAGGTGGTTCTCTCTCGACAAAAG	120
gla.sab	TTCCCTTATATTTGGGACAACACTTGTAGAATGAATCTGAGGAGGCTTTCTCTCTGATAAAG	120
gla.vol	TTCCCTTATATTTGGTACACACTTGTAGAATGAATCTGAGGAGGCTTTCTCTCTGATAAAG	120
hyl.pha	TCCCTTACATTTGGAACAGCTCTTGTGAATGAATTTGAGGGGGATTCTCCGTAGATAAAG	120
pet.see	TCCCTTATATTTGGAACAGCTCTTGTGAATGAATTTGAGGGGGATTCTCCGTAGATAAAG	120
bel.pea	TCCCTTATATTTGGAACCTGATCTAGTAGAGTGAATCTGAGGGGGGTTTCTCAGTTGACAAAG	120
pte.mom	TCCCTTATATCGGCACCAACCTTGTGAATGGATCTGAGGTGGTTTCTCAGTTGATAAAG	120
gala.demi	TCCCATATATAGGGCCTACTCTAGTAGAATGAATCTGAGGGGGGTTTCTCCGTAGACAAAAG	120
pero.pot	TCCCATATGTTAGGTAGAACCTTGTAGAATGAATTTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.mat	TTCCCTTACATCGGTACCGGCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
gala.moh	TTCCCTTATATAGGAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
oto.gar	TTCCCTTACATAGGAACCTAGTAGAATGAATCTGAGGGGGATTCTCAGTAGACAAAAG	120
lor.bar	TTCCCTTACATCGGAACCTAACCTAGTTGAATGAATCTGAGGGGGGTTCTCAGTAGATAAAG	120
lys.cou	TCCCTTATATTTGGGACAACTAGTTGAATGAATTTGAGGGGGGTTCTCAGTAGATAAAG	120
mus	TCCCATATATTTGGAACCAACCTAGTTGAATGAATTTGAGGGGGGTTCTCAGTAGACAAAAG	120
garc	TCCCTTACATCGGAACAGACCTAGTTGAATGAATTTGAGGGGGGTTCTCAGTAGATAAAG	120
homo	TCCCATACATTTGGGACCAACCTAGTTGAATGAATTTGAGGGGGGTTCTCAGTAGATAAAG	120

dug.dug	TCCCCTACATCGGCGACCAACCTAGTGAATGAATTTGAGGGGGGATTCTCAGTAGACAACG	120
ele.max	TTCCCCTACATCGGCGACCAACCTAGTGAATGAATTTGAGGGGGGCTTTTCGGTAGATAAAG	120
afr.con	TCCCCTATATTGGTCAAAACCTAGTGAATGGGCGTGAGGAGGATTCTCAGTTGACAACC	120
pavo.mut	TCCCCTATATTGGGACAAACCTAGTGAATGAGCCTGAGGGGGGATTCTCAGTCGACAACC	120
tra.bly	TCCCATACATTGGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTTGACAATC	120
tra.sat	TCCCATACATTGGTCAAAACCTAGTGAATGAACCTGAGGGGGGCTTTTCAGTTGACAATC	120
tra.cob	TCCCATACATTGGGCGAAACCTAGTGAATGGGCGTGAGGGGGGCTTTTCAGTTGACAATC	120
tra.tem	TCCCATACATTGGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTCGACAACC	120
arg.arg	TCCCCTATATTGGGACAAACCTAGTGAATGAGCCTGAGGGAGGATTCTCAGTTGACAATC	120
cat.wal	TCCCCTACATCGGACAGACCCCTAGTGAATGAGCCTGAGGGGGGATTCTCAGTTGACAACC	120
cro.cro	TCCCCTACATTTGGACAAACCTAGTGAATGAGCCTGAGGGGGGATTCTCAGTTGACAACC	120
sym.ree	TCCCCTACATCGGACAAACCTAGTGAATGAGCCTGAGGGGGGATTCTCAGTAGACAACC	120
bam.tho	TTCCCCTACATCGGACAAACCTAGTGAATGAGCCTGAGGGGGGATTCTCAGTAGATAACC	120
fra.fra	TTCCCCTACATTTGGACAAACCTAGTGAATGAGCCTGAGGGAGGATTCTCAGTAGACAACC	120
ith.cru	TTCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
ant.par	TCCCATATATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGATAATC	120
ant.vir	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.ant.ant	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.ant.gil	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.ant.sha	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.leu	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.can.pra	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.can.row	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.can.tab	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.can.can	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.ame	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.gru	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.mon	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.nig	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
gru.jap	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
cic.boy	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
rhe.ame	TCCCCTACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
ant.alb	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
fal.fam	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
fal.ver	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
fal.per	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
fal.spa	TCCCATATATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
ayc.ame	TCCCATACATCGGCGAAACCTAGTGAATGAGCCTGAGGGGGGCTTTTCAGTAGACAATC	120
smi.sha	TTCCCATACATCGGACAAACCTAGTGAATGAGCCTGAGGGAGGATTCTCAGTAGACAACC	120
vid.cha	TTCCCATACATTGGGCGAAACCTAGTGAATGAGCCTGAGGGAGGATTCTCAGTAGACAACC	120
chry.pic	TCCCATTCAATTGGTAACACATTAGTACAATGAATCTGAGGTGGATTCTCAGTAGACAACC	120
emy.orb.kur	TCCCATACATTGGCAATACACTAGTGAATGAATCTGAGGGGGGCTTTTCAGTAGACAATC	120
che.mud	TCCCATACATCGGCGAAACCTAGTGAATGAATCTGAGGGGGGCTTTTCAGTAGACAATC	120
eum.egr	TTCCATACATTGGCGACCAACCTAGTGAATGAATTTGAGGGGGGCTTTTCAGTAGACAATC	120
* * * * *		
aep.mel	CAACCCCTNACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
ore.ore	CAACCCCTTACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
add.nas	CAACCCCTTACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
ory.dam	CAACCCCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
hip.equ	CAACCCCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
alo.bus	CAACCCCTTACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
sig.lis	CAACCCCTTACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
bea.hun	CAACCCCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
dum.lun	CAACCCCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
con.hur	CAACCCCTTACCCGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
amm.les	CTACTCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130
pus.nay	CAACCCCTCACCCTGATTTTTCGGCTTCCACTTCATCTTCCATTTCATCATTTGCGGGGACTAG	130

cap.ibe	CGACTCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTAACAGCCCTCG	130
hem.jem	CTACCCTAACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTTGCAGCCCTCG	130
cap.fal	CGACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTTGCAGCCCTCG	130
rup.pyr	CTACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTTGCAGCCCTAG	130
rup.rup	CTACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTTGCAGCCCTAG	130
nam.cau	CTACTCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTTACAGCTACTG	130
bud.tax.tak	CATCCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTCG	130
pan.hod	CTACCCTAACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
ovi.amm	CGACCCTGACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
ovi.vig	CTACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
cap.cri	CGACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCAGAGCCCTCG	130
ovi.mos	CGACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGTAGCCCTCG	130
ore.ame	CTACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTCG	130
cep.dor	CAACTCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTCG	130
cep.max	CAACCCTCACTCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTG	130
bis.bon	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCAGCAATTG	130
bos.gru	CAACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTCG	130
bos.tra	CAACCCTAACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
bub.min	CAACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
buba.bub	CAACCCTCACCCGATTCTTCCGCTTCCACTTCATCTCCCATTCATCATTCGCAGCCCTCG	130
tra.ang	CAACCCTAACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCAGCCCTTG	130
tra.eur	CAACCCTAACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCAGCACTAG	130
kob.ell	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
kob.meg	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
red.aru	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
red.sul	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
neo.mos	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
pel.cap	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
gas.dam	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
our.our	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
ant.cer	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
sai.tat	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mad.kir	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
rap.mel	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
gas.gaz	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
ant.ame	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
hyd.ine	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mun.mun	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
alc.alc	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.ela.kan	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.ela.xan	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.ela.can	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.nip.cen	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.nip.yes	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.nip.ker	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.nip.pul	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.nip.nip	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.ela.sto	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
cer.dam	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
ran.tar	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mos.sus	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mos.leu	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mos.shr	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mos.ber	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
mos.mos	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
tra.jay	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
tra.gap	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130
tra.tra	CAACCCTTACCCGATTCTTCCGCTTCCACTTCATCTCCCATTTATCATTCGCAGCCCTTATTA	130

hipp.amp	CCACCCCTTACACGATTCTTTGGCCTTCCACTTTATTCTTCCATTCTTATCAGCAGCACTAG	130
dic.sum	CCACCCCTCACCCTGTTCTTTGGCTTTCCACTTCATCTCTCCCTTCATCATCTAGCCCTAG	130
rhin.son	CTACCCCTTACCCGATTCTTTGGCTTTCCACTTCATCTCTCCCTTCATCATCTAGCCCTAG	130
cera	CCACACTTACACGATTCTTTGGCCTTTCCACTTTATTCTACCCCTTTATCATCAGCCCTGG	130
equu	CCACCCCTTACCCGATTCTTTGGCCTTTCCACTTTATTCTACCCCTTTATCATCAGCCCTGG	130
baby.bab	CAACCCCTCAGACGATTCTTTGGCTTTCCACTTTATTCTACCCCTTCATCATCAGCCCTGG	130
phac.afr	CAACTCTCAGACGATTCTTTGGCCTTTCCACTTTATTCTACCCCTTCATCATCAGCCCTGG	130
sus.bar	CAACCCCTTACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTCAATTACCGCCCTGG	130
sus.scr.ewb3	CAACCCCTCAGACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATTAACCGCCCTGG	130
lama.gla	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTATTCTTACCTTTTGTCAATTGCAGCTCTAG	130
lama.gua	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTATTCTTACCTTTTGTCAATTGCAGCTCTAG	130
vic.vic	CCACCCCTTACACGATTCTTTGGCCTTTCCACTTTATTCTTACCTTTTGTCAATTGCAGCTCTAG	130
cam.bac	CCACCCCTCAGACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTTATTATCAGCGCCCTAG	130
arc.for	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCGTAGCATCAGCACTAG	130
arc.gaz	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGCATCAGCACTAG	130
eum.jub	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGCATCAGCACTAG	130
sal.cal	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGCATCAGCACTAG	130
odo.ros	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTCGTCTCTTCCATTTCATGGCATTAGCACTAA	130
pho.fasciata	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTTACCATTTGTAGTATCAGCACTAG	130
pho.gro	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTCATCTTACCATTCGTAGTATCAGCACTAG	130
pho.vit	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTCATCTTACCATTCGTAGTATCAGCACTAG	130
cys.cri	CAACTCTAACACGATTCTTTGGCCTTTCCACTTCATCTTACCATTCGTAGTATCAGCACTAG	130
hyd.lep	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGTATCAGCACTAG	130
lep.wed	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGTATCAGCACTAG	130
mir.leo	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTTACCATTCGTAGCACTAGCACTAG	130
eri.bar	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTTACCATTCGTAGTATCAGCACTAG	130
mon.sch	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTTACCATTCGTAGTATCAGCACTAG	130
hela.mal	CGACTCTAACACGATTCTTTGGCCTTTCCACTTCGTCTCTTCCATTTCATCATCTTGGCACTAA	130
sel.thi	CAACCCCTAACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCGTAGTATCAGCACTAG	130
ail.ful	CAACTCTAACACGATTCTTTGGCCTTTCCACTTCATCTTCCATTTCATTATCTCAGCCCTAG	130
fel	CCACCCCTAACACGATTCTTTGGCCTTTCCACTTCATCTTCCATTTCATTATCTCAGCCCTAG	130
can	CAACCCCTAACACGATTCTTTGGCATTCCGATTTCATCTGCCCCTTCATCATCGCAGCTCTAG	130
tal	CGACACTCAGACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTTATTATTGCGGCACTAG	130
gla.sab	CTACCCCTAACCCTGATTCTTTGGCATTTCGACTTCATTCTTCTTTTATTATTGCTTCCCTAG	130
gla.vol	CTACCTTAACCCTGATTCTTTGGCATTTCGACTTCATTCTTCTTTTATTATTGCGGCACTAG	130
hyl.pha	CTACCCCTAACCCTGATTCTTTGGCATTTCGACTTTCTGCTGCCCCTTTATTATTGCGGCACTAG	130
pet.sec	CTACCCCTAACCCTGATTCTTTGGCATTTCGACTTTCTGCTGCCCCTTTATTATTGCGGCACTAG	130
bel.pea	CAACCCCTAACACGATTCTTTGGCATTTCGACTTTATTCTTACCATTTATCGTAGCAGCCCTTG	130
pte.mom	CTACCCCTAACACGATTCTTTGGCATTTCGACTTTCTGCTGCCCCTTCATTATCGCAGCCCTAG	130
gala.demi	CTACCCCTTACCCGATTCTTTGGCTTTCCACTTTATTCTGCCCCTTTATTATCAGCAGCACTAG	130
pero.pot	CTACCCCTAACACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTTATTATCAGCAGCACTAG	130
gala.mat	CGACCCCTTACTCGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTTATTATTCAGCAGCACTAG	130
gala.moh	CTACTCTTACCCGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTTATTATTCAGCAGCACTAG	130
oto.gar	CAACCCCTCACCCTGTTCTTTGGCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
lor.tar	CAACCCCTCAGACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCATCATCGCAGCCCTAG	130
nyd.cou	CCACACTCAGACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCATCATCGCAGCCCTAG	130
mus	CGACCTTACACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCATCATCGCAGCCCTAG	130
gort	CTACCCCTTACACGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
homo	CCACCCCTCAGACGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCATCATCGCAGCCCTAG	130
dug.dug	CCACCCCTCAGCTGATTCTTTGGCCTTTCCACTTCATCTGCCCCTTCATCATCGCAGCCCTAG	130
ele.max	CAACCCCTAACCCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
afr.son	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
pavo.mut	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
tea.bly	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
tea.gat	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
tea.cob	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
tea.tem	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130
tea.ayg	CAACCCCTCAGCTGATTCTTTGGCCTTTCCACTTTATTCTGCCCCTTCATCATCGCAGCCCTAG	130

[illegible]

aap.mel	CCATAGTCCACCTACTCTTTCTCCACGAAACAGGATCTTAACAAACCCCTACAGGAATCTTCAT	240
ore.ore	CCATAGTACACCTACTCTTTCTCCACGAAACAGGCTCCAAATAACCCACAGGAATCTTCAT	240
add.nas	CCATAGTCCATCTACTCTTTCTCCACGAAACAGGCTCCAAACAAACCCCTACAGGAATCTTCAT	240
ory.dam	CCATAGTCCACCTACTCTTTCTCCACGAAACAGGCTCCAAACAAACCCCTACAGGAATCTTCAT	240
his.equ	CCATAGTACACCTACTCTTTCTCCATGAGACAGGCTCCAAACAAACCCACAGGAATTTGCAT	240
alc.bus	CCATAGTTTACCTCTTTATTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATCTTCAT	240
sig.lic	CCATAGTTTACCTCTTTATTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATCTTCAT	240
bea.hun	CCATAGTCCACCTCTTTATTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATCTTCAT	240
dam.lun	CCATAGTCCACCTCTTTATTTCTCCATGAACACAGGATCTTAACAAACCCACAGGAATCTTCAT	240
con.sau	CTATAGTCCATCTCTTATTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATTTTCAT	240
amm.les	CCATAGTCCACCTACTCTTTCTCCATGAACACAGGATCTTAACAAACCCACAGGAATTTTCAT	240
pse.nay	CCATAGTCCACCTACTCTTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATTTTCAT	240
cap.ibe	CCATAGTCCACCTCTCTTTCTCCACGAAACAGGATCTTAACAAACCCACAGGAATTTTCAT	240
hem.jem	CCATAGTCCACCTCTCTTTCTCCACGAAACAGGCTCCAAACAAACCCCAACAGGGAATTCAT	240
cup.fal	CCATAGTCCACCTACTCTTTCTCCACGAAACAGGATCTTAACAAATTCACAGGAATTTTCAT	240
cup.pyt	CCATAGTCCACCTACTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240
cup.cup	CCATAGTCCACCTACTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240
hem.cau	CTATAGTCCACCTACTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240
bus.tak.tak	CCATAGTCCACCTTTATTTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240
pan.hod	CCATAGTCCACCTTTATTTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240
avl.amm	CCATAGTCCACCTTTATTTCTTTCTCCATGAACACAGGATCTTAACAAACCCCAACAGGGAATTCAT	240

ovi.vig	CTATAGTTCACCTACTCTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTCCAT	240
cap.cri	CCATAGTGCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCCAT	240
ovi.mos	CTATAGTACATTTGCTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTCCAT	240
ore.ame	CCATAGTCCACCTACTTTTTCTCCACGAAACAGGATCTAATAACCCACAGGAATTTCAT	240
cep.dor	CCATAGTTCACCTACTCTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cep.max	CCATAGTCCACCTACTTTTTCTCCACGAAACAGGATCTAATAACCCACAGGAATTTCAT	240
bis.bon	CCATAGTTCACCTACTTTTTCTCCACGAAACAGGATCTAATAACCCACAGGAATTTCAT	240
bos.gru	CCATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAATCCAACAGGAATTTCAT	240
bos.tra	CAATAATCCATCTACTCTTCTCCACGAAACAGGATCCAACAATCCAACAGGAATTTCAT	240
bub.min	CAATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
buba.bub	CAATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
tra.ang	TTATGGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
tra.eur	CCATGGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
kob.ell	CCATAGTCCATCTTCTCTTCTCCACGAAACAGGATCCAATAATCCACAGGAATTTCAT	240
kob.meg	CTATAGTTCACCTACTTTTTCTCCACGAAACAGGATCTAACAACCCACAGGAATTTCAT	240
red.aru	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
red.ful	CTATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
neo.mos	CCATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
pal.cap	CCATAGTACACCTACTTTTTCTCCACGAAACAGGATCTAATAACCCACAGGAATTTCAT	240
gas.dam	CCATAGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
our.our	CCACAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
ant.cer	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCTAACAACCCACAGGAATTTCAT	240
sai.tat	CTATAGTCCACCTACTTTTTCTCCACGAAACAGGATCTAACAACCCACAGGAATTTCAT	240
mad.kir	CCATGGTTCACCTCTCTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
rap.mel	CTATAGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
gas.gas	CTATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
ant.ame	CCATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
hyd.ine	CCATAGTGCACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
mun.mun	CTATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
alc.alc	CCATAGTCCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.ela.kan	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
cer.ela.xan	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
cer.ela.can	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
cer.nip.cent	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.nip.yes	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.nip.ker	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.nip.pul	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.nip.nip	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
cer.ela.sco	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
cer.dam	CTATAGTACACCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
ran.tar	CTATAGTCCATTTGCTTTTTCTCCACGAAACAGGATCTAACAATCCAACAGGAATTTCAT	240
mos.fus	CTATGGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
mos.leu	CTATGGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
mos.chr	CTATGGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
mos.ber	CTATGGTTCACCTACTTTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATTTCAT	240
mos.mos	CCATGGTTCATCTACTTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
tri.jav	TCCTAGTCCACCTTTTTATTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
trig.nap	CCCTAGTCCACCTTTTTATTTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.azu	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.bon	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.bor	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.edi	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
esph.fro	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.mus	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
meg.fov	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
bala.phy	CAATTGTCCACCTCAATTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
dip.mir	CAAGCTTTTCATCTTTTCTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240
esph.com	CAAGCTTTTCATCTTTTCTTTCTCCACGAAACAGGATCCAATAACCCACAGGAATTTCAT	240

ceph.eut CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lage.obl CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
ceph.hep CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
ceph.hec CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lage.aus CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lage.cru CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lage.obs CAGCCGTCACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lisso.bor CAGCTGTTACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lisso.per CAGCTGTTACCTACTATTCTACACGAGACAGGATCCAATAACCCCCACAGGAATCCCAT 240
glo.mac TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCATAGGAATCCCAT 240
glo.mel TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
fere.att TAGCTGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
pepo.ele TAGCTGTCCACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
gram.gri TAGCTGTTACCTACTATTCTACACGAGACTGGATCCAATAACCCCCACAGGAATCCCAT 240
pse.cra CAGCTGTTACCTGCTATTCTACACGAGACAGGATCCAATAACCCCCACAGGAATCCCAT 240
lage.acu CAGCTGTTACCTGCTATTCTACACGAGACAGGATCCAATAACCCCCACAGGAATCCCAT 240
orci.bre CAGCTGTTACCTACTATTCTACACGAGACAGGATCCAATAACCCCCACAGGAATCCCAT 240
orca.bre TAAGTGTTCACCTACTATTCTACACGAAACAGGATCCAACAATCCTACAGGAATCCCAT 240
del.cap CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
del.tro CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
del.del CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sten.cly CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sten.coe CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
tur.adu CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sten.fro CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
saus.chi TAGCCGTTACCTACTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sten.lon CAGCCGTTACCTACTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
turs.tru TAGCTGTTACCTACTATTCTACACGAGACAGGATCCAACAACCCCCACAGGAATCCCAT 240
lage.alb CAAGTGTCCACCTACTATTCTACACGAGACAGGATCCAACAATCCCACAGGAATCCCAT 240
sten.bre CAGCCGTTACCTGCTATTCTACACGAAACAGGATCCAATAATCCCACAGGAATCCCAT 240
sota.flu TAGCCGTTCCATTTATTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
del.leu TGGCCGTTCCACTTATTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
mono.mon CAATTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCCCACAGGAATCCCAT 240
plat.gan CAGTTATCCACCTACTATTCTACACGAAACAGGCTCAAACAACCCCCACAGGAATCCCAT 240
plat.min CAATGGTCCACCTCTTATTCTCCACGAAACAGGATCCAACAACCCCCATAGGAATCCCAT 240
kogi.bre CAATAATCCACCTCTTATTCTCCACGAAACAGGATCCAACAACCCCCCTAGGAATCCCAT 240
kogi.sim CAATAGTACATCTCTATTCTCCATGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
phys.cat CAACCGTCCACTTACTATTCTCCATGAAACAGGATCCAACAACCCCCATAGGAATCCCAT 240
lipo.vex TAATCGTCCATCTACTATTCTCCATGAAACAGGCTCCAACAATCCCACAGGAATCCCAT 240
phoc.sin CAGCCGTTCCACTTACTATTCTCCACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
bera.bai CAGCCGTTCCACTTACTATTCTCCACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
ziph.car CAATCGTCCACTTACTATTCTCCATGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
meso.eur CAATGGTCCACCTACTATTCTCCATGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
meso.bid CAATGGTCCACCTACTATTCTCCATGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
meso.den CAATCGTCCACCTACTATTCTCCATGAAACAGGATCCAACAATCCCACAGGAATCCCAT 240
hype.amp CAATTGTCCATTTACTATTCTACACGAAACAGGATCTAATAATCCCACAGGAATCCCAT 240
meso.per TTATAGTCCACCTGCTATTCTACACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
pont.bla CCGCCGTTCCACCTACTATTCTCCACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
hex.lib CCATCGTCCATCTACTATTCTCCATGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
hipp.amp CAATTACCCACCTACTATTCTACATGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
dic.sum GAATCACCACCTTACTATTCTACACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
rhin.son GAATCACCACCTTACTATTCTTCAAGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
cata TAATCGTCCATCTACTATTCTCCACGAAACAGGATCCAACAACCCCCACAGGAATCCCAT 240
equu GAACCGTACATCTATTATTCTTCCACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
baby.bab GAACCGTACATCTATTATTCTTCCACGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
phac.afr CAGCCGTTACATCTCTATTCTTCAAGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sus.bac CAGCCGTTACATCTCTATTCTTCAAGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240
sus.scc.95b CAGCCGTTACATCTCTATTCTTCAAGAAACAGGATCCAATAACCCCCACAGGAATCCCAT 240

gru.ant.gil	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.ant.sha	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.leu	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.can.pra	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATTGTAT	240
gru.can.row	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAATCCCCCTAGGCATTGTAT	240
gru.can.tab	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATTGTAT	240
gru.can.can	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATTGTAT	240
gru.ame	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.gru	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.mon	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.nig	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
gru.jap	CCCTAATCCACCTCAGCTTCCTTCACGAAATCCGGGCTCAAACAACCCCCCTAGGCATCGTAT	240
cic.boy	CCCTAATCCACCTCAGCTTCCTTCACGAGTCCGGGCTCAAACAACCCCCCTAGGCATCATCT	240
rhe.ame	CCTTTATCCACCTCAGCTTCCTTCACGAAACCGGGTCCAACAACCCCCCTAGGAATCGTAT	240
ant.alb	TCCTAATTCACCTGGCATTCTCTCACGAAATCAGGCTCAAACAACCCACTAGGCATCAGAT	240
fal.fam	CCCTAATCCACCTCAGCTTCCTTACATGAATCAGGTTCAAACAACCCCCCTAGGAATCAGAT	240
fal.ver	CCCTAATTCACCTCAGCTTCCTTACGAAATCAGGTTCAAACAACCCCCCTAGGAATCAGAT	240
fal.per	CCCTAATCCACCTCAGCTTCCTTACATGAATCAGGTTCAAATAACCCCCCTAGGAATCAGAT	240
fal.spa	CCCTAATCCACCTCAGCTTCCTTACATGAATCAGGTTCAAACAACCCCCCTAGGAGTCAGAT	240
ayt.ame	CCCTAGTCCACCTAACTTTCCTGCACGAGTCAGGTTCAAACAACCCCCCTAGGCATTGTAT	240
smi.sha	CAGTCATCCATCTCAGCTTCCTTCATGAAACAGGTTCAAACAACCCCTCTAGGTATCTCAT	240
vid.cha	CTCTAGTCCACCTCAGTTCTTACACGAAACAGGATCAAACAATCCATAGGAATTCCAT	240
chry.pic	CAATAGTACACCTACTTTTCTTACATGAAACTGGATCAAACAACCCCAACAGGATTAAACT	240
emy.orb.kur	CAATAGTACACCTACTCTTCTTACACGAAACCGGATCAAACAATCCCAACAGGATTAAACT	240
che.mud	CAGCAGTACATCTATTATTCTTCTGCACGAAACAGGATCAAACAACCCCAACAGGATTAAAT	240
eum.egr	CAATAATTACCTACTATTCTTCTTACGAAACAGGATCAAATAACCCCAACCGGACTAAATT	240

aep.mel	CAGATTGAGATAAAAATTCGATTCCACCCTTACTATACCTATTAAAGACATCCTAGGAATCC	300
ore.ore	CAGACACAGACAAAAATCCGATTTCATCCTTATTACGCAATCAAGATATCCTAGGCGCCC	300
add.nas	CAGACACAGACAAAAATCCGATTTCACCCTTACTATACCATTTAAAGACATCCTAGGCGCCC	300
ory.dam	CAGACACAGACAAAAATTCGGTTCCACCCTTATTATACCATTTAAAGATATCCTAGGCGCCC	300
hip.equ	CAGACTCCGATAAAAACCCGATTCCACCCTTACTACACCATTTAAAGACATTCTAGGCGCCC	300
alc.bus	CAGACCGAGATAAAAATCCGATTCCACCCTTACTATACCAATCAAGGACATTCTAGGCGCCC	300
sig.lic	CAGACCGAGATAAAAATCCGATTCCACCCTTACTATACCAATCAAGGACATTCTAGGCGCCC	300
bea.hun	CAGATGCAGATAAAAATTCGATTCCACCCTTACTACACCATTTAAAGACATCCTAGGCGCCC	300
dam.lun	CAGATGCCGACAAAAATCCGTTTCACCCTTACTACCATTTCAAGACGCCCCTAGGGGCCC	300
con.tau	CCGACACCGATAAAAATCCGATTTCGCCCCCTATTACACCATTTAAAGACATCCTAGGCGCTC	300
amm.les	CAGACCGAGACAAAAATCCGATTTCACCCTTACTACACCATTTAAAGATATTCTAGGCGCCA	300
pse.nay	CAGACACAGACAAAAATCCGATTTCACCCTTACTACACCATTTAAAGATATTCTAGGCGCTG	300
cap.ibe	CAGACACAGACAAAAATCCGATTTCACCCTTACTACACCATTTAAAGATATCCTAGGCGCCA	300
hem.jem	CAGATACAGACAAAAATCCGATTTCCACCCTTACTACACCATTTAAAGATATTTTAGGCGCCA	300
cap.fal	CAGACACAGACAAAAATCCGATTTCCACCCTTACTACACCATTTAAAGATATCCTAGGCGCCA	300
rup.pyr	CAGATGCCGATRAAAATCCGATTTCCACCCTTACTATACCATTTAAAGACATTCTAGGCGCCA	300
rup.rup	CAGATGCCGACAAAAATCCGATTTTACCCTTATTATACCATTTAAAGACATTCTGGGCGCCA	300
nem.gau	CAGACATAGACAAAAATCCGATTTCCACCCTTATTATACCAATCAAGATATTCTAGGCGCTA	300
bud.tax.tax	CAGATGCAGATAAAAATTCGATTTCCACCCTTATTACACCATTTAAAGATATCCTAGGAGTCA	300
pan.hod	CAGATGCAGACAAAAATCCGATTTCCACCCTTACTATACCATTTAAAGACATCCTAGGCGCTA	300
ovi.amm	CGGACACAGATAAAAATTCGCTTCCACCCTTACTACACCATTTAAAGACATCCTAGGCGCCA	300
ovi.vig	CGGACACAGACAAAAATCCGCTTCCACCCTTCCNNRRRRRRRRNNIATTTAAAGACATTCTGGGTGCCA	300
cap.cri	CAGACACAGACAAAAATCCGATTTCCACCCTTACTACACCAATCAAGATATCCTAGGCATCG	300
ovi.mos	CAGACACGGACAAAAATCCGATTTCCACCCTTACTATACCAATCAAGACATTCTAGGCGCCA	300
ore.ame	CAGACCGAGACAAAAATTCGATTTCCACCCTTACTATACCATTTAAAGATATCCTAGGCGCCA	300
cep.dor	CGGACCGAGACAAAAATTCGATTTCCACCCTTACTATACCATTTAAAGACATCCTAGGCGCCC	300
cep.max	CAGACCGAGACAAAAATTCGCTTCCACCCTTACTACACCATTTAAAGACATCCTAGGCGCCC	300
bis.bon	CAGACACAGACAAAAATTCGATTTCCACCCTTACTATACCATTTAAAGACATCCTAGGAGCCT	300
bot.gcu	CAGACCGAGACAAAAATTCGATTTCCACCCTTACTATACCATTTAAAGACATCCTAGGAGCCT	300
bot.gsa	CAGACCGAGATAAAAATCCGATTTCCACCCTTACTATACCATTTAAAGACATCCTAGGAGCCT	300

bub.min	CAGACACAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGCGCCC	300
buba.bub	CAGACACAGACAAAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGCGCCC	300
tra.ang	CAGACATAGACAAAATCCCATTTCCACCCCTATTACACTATCAAGGACATCCTAGGCGCCC	300
tra.eur	CRAACATAGACAAAATCCCATTTCCACCCCTACTACACTATTAAGGACATCCTAGGCGCCC	300
kob.ell	CAGACATAGATAAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGCGCCC	300
kob.meg	CAGACACAGACAAAATCCCATTTCCACCCCATATTATACCATCAAGATATTTCTAGGCGCCC	300
red.aru	CAGATGTAGACAAAATCCCATTTCCATCCCTACTATACCTATCAAGGACGTTCTAGGCGCCC	300
red.ful	CAGAYATGGACAAAATCCCATTTCCACCCNTACTACACCAATCAAGAYATTTCTAGGCGCCC	300
neo.mos	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGCGCCC	300
pel.cap	CCGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGATATTTCTAGGCGCCC	300
gaz.dam	CAGATGCAGACAAAATCCCGTTTCCACCCCTACTACACCAATCAAGACATTCTAGGAGCAC	300
our.our	CAGATGCAGACAAAGTCCCATTTCCACCCCTACTACACTATCAAGATATCCTAGGAGCTC	300
ant.cer	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGCGCCC	300
sai.tac	CAGATTGAGACAAAATCCCATTTCCACCCCTACTACACTATTAAGACATCCTAGGCGCCC	300
mad.kir	CAGACGCAGACGGAATCCCATTTCCGCCCCCTACTACACTATTAAGACATCCTAGGCGCCC	300
rap.mel	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGAGCCC	300
gaz.gaz	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGGACATTCTAGGAGCAC	300
ant.ame	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGAGCAC	300
hyd.ine	CAGATGCAGATAAAAATCCCATTTCCATCCCTACTACACCAATTAAGATATTTCTAGGTGTAC	300
mun.mun	CAGATGTAGACAAAATCCCATTTCCATCCCTACTATACCATTAAGATATTTCTAGGTGCCC	300
alc.alc	CAGACGCAGACAAAATCCCATTTCCACCCCTACTACACTATCAAGATATCTTAGGTGCCC	300
cer.ela.kan	CAGACGCAGACAAAATCCCGTTTCCATCCTTACTATACCATTAAGATATCTTAGGCATCT	300
cer.ela.xan	CAGACGCAGACAAAATCCCGTTTCCATCCTTACTATACCATTAAGATATCTTAGGCATCT	300
cer.ela.can	CAGACGCAGACAAAATCCCGTTTCCATCCTTACTATACCATTAAGATATCTTAGGCATCT	300
cer.nip.cent	CGGACGCAGACAAAATCCCGTTTCCATCCTTACTACACCAATTAAGATATCTTAGGCATCT	300
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cer.nip.ker	CGGACGCAGACAAAATCCCGTTTCCATCCTTACTATACCATTAAGATATCTTAGGCATCT	300
cer.nip.pul	CGGACGCAGACAAAATCCCGTTTCCATCCTTACTATACCATTAAGATATCTTAGGCATCT	300
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cer.ela.sco	CAGACGCAGACAAAATCCCGTTTCCATCCTTATTATACCATTAAGATATCTTAGGCATCT	300
cer.dam	CAGATGTAGATAAAAATCCCGTTTCCATCCTTACTACACCAATTAAGATATTTTAGGCATCC	300
ran.tar	CAGACTCAGATAAAAATCCCATTTCCATCCTTATTATACCTATCAAGACATTCTAGGTGTCC	300
mos.fus	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGTGTCC	300
mos.leu	CAGATATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGTGTCC	300
mos.chr	CAGACATAGACAAAATCCCATTTCCACCCCTACTACACTATCAAGACATTCTAGGTGTCC	300
mos.ber	CAGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGATATTTCTAGGTATCC	300
mos.mos	CAGACGCAGACAAAATCCCGTTTCCACCCCTACTACACTATTAAGACATTCTAGGGGTTCC	300
tra.jav	CAGACGCAGACAAAATCCCGTTTCCACCCCTACTACACTATTAAGACATTCTAGGGGTTCC	300
trag.nap	CAGACGCAGACAAAGATCCCGTTTCCACCCCTACTACACCAATCAAGATGTCTAGGGGTTCC	300
bala.acu	CTGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGGGTTCC	300
bala.bon	CTGATATAGACAAAATCCCATTTCCACCCCTATTACACCAATCAAGACATTCTAGGGGTTCC	300
bala.bor	CCGACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGGGTTCC	300
bala.edi	CCAACATAGACAAAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
esch.rob	CCAACATAGACAAAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
bala.mus	CTGACATAGATAAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGGGTTCC	300
mega.nov	CCAACATAGACAAAATCCCATTTCCACCCCTACTACACCAATCAAGACATTCTAGGGGTTCC	300
bala.phy	CCGACATAGATAAAAATCCCATTTCCACCCCTACCACACCAATTAAGACATTCTAGGGGTTCC	300
cap.mar	CCAACATAGACAAAATCCCATTTCCACCCCTACTACACCAATTAAGACATTCTAGGGGTTCC	300
ceph.com	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
ceph.eut	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
lage.obl	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
ceph.heu	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
ceph.heu	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
lage.aus	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
lage.sru	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
lage.sbs	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
liso.bor	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300
liso.por	CCAACATAGACATAATCCCATTTCCACCCCTATTACACCAATTAAGACATTCTAGGGGTTCC	300

glo.mac	CCAACATAGACATAAATTC	300
glo.mel	CCAACATAGACATAAATTC	300
fere.att	CCAACATAGACATAAATTC	300
pepo.ele	CCAACATAGACATAAATTC	300
gram.gri	CCAACATAGACATAAATTC	300
pse.cra	CCAACATAGACATAAATTC	300
lage.acu	CCAACATAGACATAAATTC	300
orci.bre	CCAACATAGACATAAATTC	300
orca.bre	CCAACATAGACATAAATTC	300
del.cap	CCAACATAGACATAAATTC	300
del.tro	CCAACATAGACATAAATTC	300
del.del	CCAACATAGACATAAATTC	300
sten.cly	CCAACATAGACATAAATTC	300
sten.coe	CCAACATAGACATAAATTC	300
tur.adu	CCAACATAGACATAAATTC	300
sten.fro	CCAACATAGACATAAATTC	300
saus.chi	CCAACATAGACATAAATTC	300
sten.lon	CCAACATAGACATAAATTC	300
turs.tru	CCAACATAGACATAAATTC	300
lage.alb	CCAACATAGACATAAATTC	300
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sota.flu	CCAACATAGACATAAATTC	300
del.leu	CCAACATAGACATAAATTC	300
mono.mon	CCAACATAGACATAAATTC	300
plat.gan	CCAACATAGACATAAATTC	300
plat.min	CCAACATAGACATAAATTC	300
kogi.bre	CCAACATAGACATAAATTC	300
kogi.sim	CCAACATAGACATAAATTC	300
phys.cat	CCAACATAGACATAAATTC	300
lipo.vex	CCAACATAGACATAAATTC	300
phoc.sin	CCAACATAGACATAAATTC	300
bera.bai	CCAACATAGACATAAATTC	300
niph.car	CCAACATAGACATAAATTC	300
meso.eur	CCAACATAGACATAAATTC	300
meso.bid	CCAACATAGACATAAATTC	300
meso.den	CCAACATAGACATAAATTC	300
hype.amp	CCAACATAGACATAAATTC	300
meso.per	CCAACATAGACATAAATTC	300
pent.bla	CCAACATAGACATAAATTC	300
hex.lib	CCAACATAGACATAAATTC	300
hipp.amp	CCAACATAGACATAAATTC	300
dic.sum	CCAACATAGACATAAATTC	300
rhin.son	CCAACATAGACATAAATTC	300
cera	CCAACATAGACATAAATTC	300
equu	CCAACATAGACATAAATTC	300
baby.bab	CCAACATAGACATAAATTC	300
phac.afr	CCAACATAGACATAAATTC	300
sus.bar	CCAACATAGACATAAATTC	300
sus.ser.ewb3	CCAACATAGACATAAATTC	300
lama.gla	CCAACATAGACATAAATTC	300
lama.gua	CCAACATAGACATAAATTC	300
vic.vic	CCAACATAGACATAAATTC	300
cam.bac	CCAACATAGACATAAATTC	300
acc.foc	CCAACATAGACATAAATTC	300
acc.gac	CCAACATAGACATAAATTC	300
sum.jub	CCAACATAGACATAAATTC	300
sal.sal	CCAACATAGACATAAATTC	300
ddp.fps	CCAACATAGACATAAATTC	300

pho.fasciata	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.gro	CCGACTCAGACAAAAATCCCGCTCCACCCATACTATACAATTTAAAGATATCCTAGGAGCCC	300
pho.vit	CCAATCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATCCTAGGGGCCC	300
cys.cri	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGACATCCTAGGAGCCC	300
hyd.lep	CCAATCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACATCCTAGGAGCCC	300
lep.wed	CTGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATCTTAGGAGCCC	300
mir.leo	CCGACTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGATATCTTAGGAGCCC	300
eri.bar	CCGACTCAGATAAAAAATCCCATTTCCACCCATACTATACAGTCAAGGACATCTTAGGGGCTT	300
mon.sch	CCAATCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGACATCTTAGGAGCTT	300
hela.mal	CTGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAGGACATCTTAGGCGCCC	300
sel.thi	CCAATCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGACGCCCCTAGGCGCCC	300
ail.ful	CCAATCAGACAAAAATCCCATTTCCATCCCTATTATACAATTTAAAGATATCTTGGGCGCTC	300
fel	CCGATTCAGACAAAAATCCCATTTCCACCCATACTATACAATTTAAAGACATCCTTAGGTCTTC	300
can	CAGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGGATATCCTTAGGAGCCT	300
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gla.vol	CTGACTCAGACAAAAATCCCATTTCCACCCCTACTTTCTCAATTTAAAGATCTCCTTAGGCGCCC	300
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pet.set	CCGATTCAGACAAAAATCCCATTTCCACCCATACTATTCAATTTAAAGATCTCCTTAGGGGCCC	300
bel.pea	CTGAATCTGATAAAAGTACCATTTCCACCCCTACTTTCAATTTAAAGATATTCTTGGGCGCCC	300
pte.mom	CCGAATCCGACAAAAATCCCATTTCCACCCCTACTTTCAATTTAAAGACATTTTAGGAGCAC	300
gala.demi	CAGACTCAGACAAAAATCCCATTTCCACCCCTATTACATAATTTAAAGGATCTCCTTAGGACTGA	300
pero.pot	CAGAATCAGACAAAAATCCCATTTCCACCCCTACTATACACCACTAAAGACTTACTAGGAGCCA	300
gala.mat	CAGACTCCGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACCTACTTAGGAGTAA	300
gala.moh	CAGACTCCGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACCTACTTAGGAGCAA	300
oto.gar	CAGACTCTGACAAAAATCCCATTTCCACCCCTATTACACAATTTAAAGACCTTCTTAGGGGCTA	300
lor.tar	CAGACTCTGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATTCTTAGGAGTAA	300
nyc.cou	CAGACTCAGATAAGATTCCCATTTCCACCCCTACTACTCAATTTAAAGACCTCCTTAGGAGTGG	300
mus	CAGATGCAGATAAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGATATCCTTAGGTATCC	300
gorr	CCCACCTCTGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACATCCTTAGGCCTAT	300
homo	CCCATTCCGATAAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACGCCCCTCGGCTTAC	300
dug.dug	CCGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACCTCCTTAGGCCTAT	300
ele.max	CAGACTCAGACAAAAATCCCATTTCCACCCCTACTATACAATTTAAAGACTTCTTAGGGCTAC	300
afr.con	CCAATTCAGATAAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
pavo.mut	CCAATTCAGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAA	300
tra.bly	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAA	300
tra.sat	CCAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAA	300
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tra.tem	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAA	300
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cat.wal	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
cro.cro	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGACATCCTTAGGCCTAG	300
sym.ree	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
bam.tho	CTAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGACATCCTTAGGCCTAG	300
fra.fra	CTGACTCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGACATCCTTAGGCCTAG	300
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ant.par	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
ant.vir	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.ant.ant	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
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gru.ant.shu	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.leu	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.can.pra	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
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gru.can.tab	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.can.can	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.ame	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300
gru.gro	CAAATCTGACAAAAATCCCATTTCCACCCCTACTACTCCCTCAAAGATATCCTTAGGCCTAG	300

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 gru.nig CAAACTGCGATAAAATTCATTCCACCCCTATTTTTCTTAAAAAGATACCTAGGATTCA 300
 gru.jap CAAACTGTGATAAAATCCCATTCACCCCTATTTTTCTTAAAAAGATATCTTAGGATTTA 300
 cic.boy CAAACTGCGACAAAATTCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGCCTTA 300
 rhe.ame CTCACTCTGACAAAATCCCATTCACCCCTACTTCTCCCTCAAAGATATGCCCTAGGACTAG 300
 ant.alb CCAACTGCGACAAAATCCCATTCACCCCTACTTTGCCCTAAAGGACATCCTAGGATTCA 300
 fal.fam CAAACTGCGATAAAATTCATTCCATCCCTACTACTCTCTCAAAGACCTTTTAGGAGTCA 300
 fal.ver CAAACTGCGACAAAATCCCATTCATCCCTACTACTCTCTCAAAGACCTTTTAGGAGTCA 300
 fal.per CAAATTTGCGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGATATCCTAGGATTTA 300
 fal.spa CAAACTGTGACAAAATCCCATTCACCCCTACTACTCTCTCAAAGACCTCCTAGGTTTAA 300
 ayt.ame CAGACTGCGACAAAATCCCATTTCCACCCCTACTTCTCCTCAAAGACATCCTAGGATTTA 300
 smi.sha CTAACTCCGATAAAATTCATTCCACCCCTACTTCTCCATAAAAGACATTCTAGGCTTTG 300
 vid.cha CAGACTGTGACAAAATTCATTCCACCCCTACTACACCACAAAGGACATCCTAGGCTTCG 300
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 emy.orb.kur CAAACACCGATAAAATCCCTTTCCATCCCTACTTCTCATACAAAGACCTATTAGGACTCA 300
 che.mud CAAATACCGACAAAATCCCTTTCCACCCCTACTTCTCTACAAAGACTTACTAGGACTCA 300
 eum.egr CTAGCACAGATAAGGTGCCATTCCACCCCTATTACACATACAAAGACCTTCTTGGTTTCA 300

* ** * *

aep.mel TATTAATAATTCTAGTCCTAATCTCCTAGTACTATTTCATACCCGACCTACTAGGAGACC 360
 ore.ore TATTACTAATTCTAGCTTTTATTACTCTTAGTATTATTCACACCTGACCTACTTGGAGACC 360
 add.nas TACTACTAATTCTAGTCCTGACTACTAGTATTATTCACACCCGACCTACTTGGAGACC 360
 ory.dam TACTACTAATCCTAGCCCTTATGTTGCTAGTATTATTCGACCCGACCTACTTGGAGACC 360
 hip.equ TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTACTTGGAGACC 360
 alc.bus TATTACTAATCCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
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 bea.hun TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
 dam.lun TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
 con.tau TATTACTAATTCTAGCCCTAATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
 amm.ler TGCTACTAATCCTCACCCTCAGACTACTAGTACTATTTCACCCGACCTACTCGGGGACC 360
 pse.nay CACTGCTAATCCTCGCCCTGATATTACTAGTATTATTTACACCCGACCTACTCGGAGACC 360
 cap.ibe TGCTACTAATTCTTGCTTAATATTACTAGTACTATTTCACACCCGACCTACTCGGGGACC 360
 hem.jem TACTACTAATTCTTGCTTAATATTACTAGTACTATTTCACCCGACCTACTTGGAGACC 360
 cap.fal TACTACTAATTCTCGCCCTGATGCTACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
 rup.pyr TACTACTAATCCTCACCCTTATACTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
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 nem.cau TACTACTAATCCTCACCCTTATTTACTGGTACTATTTCACACCTGACCTACTCGGAGACC 360
 bud.tax.tax TACTACTAATCCTCAGCCCTAATCTAGTACTATTTCACCCGACCTACTCGGAGACC 360
 pan.hod TACTACTAATCCTAATCCTCATATTACTAGTACTATTTCACCCGACCTACTCGGAGACC 360
 ovi.amm TCCTACTAATCCTCACCCTCATACTACTAGTACTATTTCACCCGACCTACTCGGAGACC 360
 ovi.vig TCCTACTAATCCTCATCCTCATGCTGCTAGTACTATTTCACCCGACCTACTCGGAGACC 360
 cap.cri TGCTACTAATCCTCACCCTCATACTACTAGTACTGTTTCACACCCGACCTACTCGGAGACC 360
 ovi.mos TACTACTAATCCTTACCCTTATACTACTAGTATTATTTACACCCGACCTACTTGGAGACC 360
 ore.ame TACTACTCATCCTCACCCTTATACTACTAGTATTATTTCTCACCCTGACCTACTCGGAGACC 360
 cep.dor TACTACTCATTCTAGCCCTAATAATCCTAGTATTATTTCTCACCCTGACCTACTCGGAGACC 360
 cep.max TATTACTTATTCTAGCCCTAATAATCCTAGTACTATTTCACCCGACCTACTCGGAGACC 360
 bis.bon TATTACTAATTCTAATCTAATACTACTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
 bos.gru TATTACTAATTCTAGCCCTAATAACTTCTGCTACTATTTCACACCCGACCTCCTCGGAGACC 360
 bos.tra TACTACTTATTCTAGCCCTAATAATACTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
 bub.min TGCTATTAATCCTAGCCCTAATACTATTAGTACTATTTCACACCCGACCTCCTCGGGGACC 360
 buba.bub TACTATTAATCCTAGCCCTAATACTATTAGTACTATTTCGACCCGACCTCCTCGGGGACC 360
 tra.ang TACTATTAATCCTAGCCCTAATACTAGTACTATTTCACACCTGACCTACTCGGAGACC 360
 tra.eur TACTGCTAATCCTAGCCCTAATACTAGTACTATTTCGACCCGACCTCCTCGGAGACC 360
 kob.ell TACTACTAATCCTAGTCTAATACTCCTAGTATTATTTCCGCCCCGACCTACTTGGAGACC 360
 kob.meg TCCTATTAATCCTAATACTAATACTCCTAGTACTATTTCGCCCCGACCTACTTGGAGACC 360
 red.aru TACTGCTAATCCTAGTCTAATACTCCTAGTATTATTTACCCCTGACCTACTCGGAGACC 360
 red.ful TACTACTAATCCTGCCCCAAGACTATTAGTACTATTTCACCCCTGACCTACTCGGAGACC 360
 neo.mos TCCTACTAATTCTAGTCTAAGACTTTAGTATTATAATTCGACCTGACCTACTCGGAGACC 360

del.cap	TACTCCTAATCTTAACCCCTACTAGCACTGACCCTATTCACTCCAGACCTACTAGGAGACC	350
del.tro	TACTCCTAATCTTAACCCCTACTAGCACTGACCCTATTCACTCCCGACCTACTAGGAGACC	350
del.del	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.cly	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.coe	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
tur.adu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAAACC	350
sten.fro	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
saus.chi	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.lon	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
turs.tru	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lage.alb	TACTTTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sten.bre	TACTTTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sota.flu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
del.leu	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
mono.mon	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
plat.gan	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
plat.min	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
kogi.bre	TACTGCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
kogi.sim	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
phys.cat	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lipo.vex	TCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
phoc.sin	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
bera.bai	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
niph.car	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.eur	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.bid	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.den	TACTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
hype.amp	TATTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
meso.per	TATTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
pont.bla	TATTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
hex.lib	TACTTCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
hipp.amp	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
dic.sum	TACTTCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
rhin.son	TGCTTCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
cera	TACTCCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
equu	TGCTTCTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
baby.bab	TACTCATAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
phac.aff	TATTCTAATACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sus.bar	TATTCTAATACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sus.scr.ewb1	TATTCTAATACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lama.gla	TACTACTTATTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lama.gua	TACTACTTATTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
vic.vic	TACTACTTATTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
cam.bac	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
arc.for	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
arc.gaz	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
eum.jub	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
sal.cal	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
odo.rus	TGCTACTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
pho.fasciata	TACTCCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
pho.gro	TACTCCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
pho.vic	TACTCCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
rys.cri	TACTCCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
nyd.lep	TATTCTCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
lep.wed	TACTCCTCATCTAGCTCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
nir.leo	TACTTCTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
cri.bar	TACTTCTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350
non.ngh	TACTTCTTAATCTTAACCCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	350

hela.mal	TACTTCTTACCGTACCGCTAACAAACCGTACTTCTATTCTCGCCCCGACTTACTAGGAGACC	363
sel.chi	TACTTCTCATCGTACCGCTTACCAACTCTACTCTCTATTCTCGCCCCGACTTACTAGGAGACC	364
ail.ful	TACTCCTTATCGTAACTTCTCATGACACTAGTACTATTCTTACCTGACTTCTCTGATG	365
fel	TACTACTAGTTTAAACACTCATACTACTCTCTCTATTCTTACCCAGACCTGCTAGGAGACC	366
can	TACTCCTACTCGTAACTCTAAATATCACTAGTTTCTATTCTTACCTGACCTATTAGGAGACC	367
tal	TAATCCTAAATATAGCTCTATCATCACTTAGTATTATTCTTACCTGACCTACTAGGAGACC	368
gla.sab	TAATCCTCATCTTAACTCTTCTATAACCGTAGTTCTCTTACCCCTGACTCTTCTAGGAGACC	369
gla.vol	TAATCCTTATCTTAACTCTTCTATAACCGTAGTTCTCTTACCCCTGACTCTTCTAGGAGACC	370
hyl.pha	TTATTCTTCTCTTAACTCTTCTATAAACTTAGTACTATTCTTCTCTCTCTCTTCTAGGAGACC	371
pec.sec	TTATTCTTCTCTTAACTCTTCTATAAACTTAGTACTATTCTTCTCTCTCTCTTCTAGGAGACC	372
bel.pea	TAATCCTTCTCTCTTAACTCTTCTATAAACTTAGTACTATTCTTCTCTCTCTCTTCTAGGAGACC	373
pea.mem	TTCTCCTTCTCTCTTAACTCTTCTATAAACTTAGTACTATTCTTCTCTCTCTCTTCTAGGAGACC	374
gala.demi	TTATTCTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	375
pero.pot	TTCTTCTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	376
gala.mat	TTCTTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	377
gala.moh	TTCTTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	378
oto.gar	TTCTTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	379
lor.tar	TTCTTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	380
nyc.cou	TTCTTCTTACTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	381
mus	TAATCATATCTTAACTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	382
gorr	TTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	383
homo	TTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	384
dug.dug	TTATCCTAAATTTTACTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	385
ele.max	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	386
afr.con	CTCTTATCTTATCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	387
pavo.mut	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	388
tra.bly	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	389
tra.sac	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	390
tra.cob	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	391
tra.tem	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	392
arg.arg	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	393
cac.wal	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	394
cro.cro	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	395
sym.zee	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	396
bam.cho	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	397
fra.fra	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	398
ish.cfu	CACCTCATGCTCATCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	399
ant.par	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	400
ant.vir	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	401
gru.and.ant	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	402
gru.and.gil	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	403
gru.and.sha	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	404
gru.leu	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	405
gru.can.pra	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	406
gru.can.sow	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	407
gru.can.cab	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	408
gru.can.can	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	409
gru.ame	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	410
gru.gru	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	411
gru.mon	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	412
gru.nig	TACTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	413
gru.jap	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	414
dis.boy	CACCTCATACTACTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	415
che.ame	CTCTCATATTTATCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	416
ant.alb	CAGTAAATATCTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	417
sal.sam	TACTCATATACTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	418
sal.yes	TACTCATATACTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	419
sal.per	TACTCATATACTCTCTCTCTCTCTCTCTCTCTCTCTAGTAAATATTCTTCTCTCTCTCTTCTAGGAGACC	420

TGCTCATACTCCTGCCCTAATAGCCCTAGCCCTATTACCCCCAAACCTGCTAGGAGACC 360
 TCCTCATGCTACCCCCCTAATAGCACTAGCCCTATTCTCACCAAACCTCCTAGGAGACC 360
 CAATCATACTAACACCCACTAATAACCCCTAGCCATAATTCTCTCTTAACCTCCTAGGAGACC 360
 TACTAATAATTCCGACTCCTAGCTTCCATAGCCCTATTCTCCCCAAACATACTAGGAGATC 360
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 TCCTAATACTAGCCTTCTGCTAACCCCTAACACTATTCTCTCTTAACCTTCTAGGAGACC 360
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 TCATTATACTGTCTGTTCTACTAGCCCTCGCCCTTTTCTCACCAAACCTTCTAGGCGACC 360

[illegible]

turs.tru	CTGATAACTACACCCAGCAAAACCCACTAAGCACCCCTGCACACATCAAACCAGAAATGAT	420
lage.alb	CCGATAACTATACCCAGCAAAATCCACTAAGCACTCCTGCACACATCAAACCAGAAATGGT	420
sten.bre	CCGACAACCTATACCCAGCAAAATCCACTAAGCACCCCTGCACACATCAAACCAGAAATGGT	420
sota.flu	CCGACAACCTATACCTCCAGCAAAATCCACTTAACACCCCTGCACACATCAAACCAGAAATGAT	420
del.leu	CAGACAATTACACCCAGCAAAACCCACTAAACACCCCCCGCACACATCAAACCAGAAATGGT	420
mono.mon	CTGACAATTATACCCAGCAAAACCCACTAAGCACCCCTGCACACATCAAACCAGAAATGGT	420
plat.gan	CCGATAACTACACCCAGCAAAACCCCTTAATACCCAGCACATATCAAACCAGAAATGGT	420
plat.min	CCGATAACTACACCCAGCAAAACCCCTTAATACCCAGCACATATCAAACCAGAAATGGT	420
kogi.bre	CTGACAACCTACACCCAGCAAAACCCACTAAGCACCCCGCACACATTAACCAGAAATGGT	420
kogi.sim	CCGACAACCTATACCCAGCAAAACCCACTAAGCACCCCGCACACATTAACCAGAAATGGT	420
phys.cat	CTGACAACCTATACCCAGCAAAACCCACTAAGCACCCCGCACACATTAACCAGAAATGGT	420
lipo.vex	CTGATAATTATACCCAGCAAAACCCACTAAGCACCTCCCGCACACATCAAACCAGAAATGGT	420
phoc.sin	CCGATAACTACATTCCAGCAAAACCCACTAAGCACCCCGCACACATTAACCAGAAATGGT	420
bera.bai	CCGACAACCTATACCCCGCAAAACCCCTCAGCACCCCAACACATATTAAGCCAGAAATGGT	420
ziph.car	CCGATAACTATACCCAGCAAAATCCACTCAGCACCCCGCACACATTAAGCCAGAAATGGT	420
meso.eur	CCGACAATTACACCCAGCAAAACCCACTTAATACCTCCAGCACACATCAAACCAGAAATGGT	420
meso.bid	CCGACAACCTATACCCAGCAAAACCCACTCAGCACCCCGCACACATCAAACCAGAAATGGT	420
meso.den	CCGATAATTATACCTCCAGCAAAACCCACTCAACACTCCAGCACACATCAAACCAGAAATGGT	420
hype.amp	CTGATAACTATACCCAGCAAAACCCACTCAGCACTCCAGCACACATCAAACCAGAAATGGT	420
meso.per	CTGACAATTACACTCCAGCAAAACCCACTTAGCACCCCGCACACATTAACCAGAAATGGT	420
pont.bla	CAGACAACCTATATCCAGCAAAACCCCATGAATACCCAGAGCACATTAACCAGAAATGGT	420
hex.lib	CAGACAACCTACACCCCGCAAAACCCCTTAGCACACCACCAACATCAAACCAGAAATGGT	420
hipp.amp	CAGACAACCTACACCCCGCAAAACCCCTTAGCACACCACCAACATTAACCAGAAATGGT	420
dic.sum	CCGACAACCTACACACCCCGCAAAACCCCTCAGCACCCCTCCACACATTAACCAGAAATGGT	420
rhin.son	CAGACAACCTACATCCAGCAAAACCCCTCAGCACCCCTCCACATATCAAACCAGAAATGGT	420
cera	CTGACAACCTACACCCCTGCCAATCCTCAGCACCTCCCCACATATCAAACCAGAAATGGT	420
equu	CAGACAACCTACACCCAGCTAACCCTCAGCACCTCCCTCATATTAAGCCAGAAATGGT	420
baby.bab	CCGACAACCTATACCTCCAGCAAAACCCACTAATACACCACCCACATTAAGCCAGAAATGGT	420
phac.afr	CAGACAACCTATACCCAGCAAAACCCATTAACACACCACCCACATCAAACCAGAAATGGT	420
sus.bar	CAGACAACCTACACCCAGCAAAACCCACTAAGCACCCACCCCATATTAACCAGAAATGGT	420
sus.scr.ewb3	CAGACAACCTACACCCAGCAAAACCCACTAAGCACCCACCCCATATTAACCAGAAATGGT	420
lama.gla	CCGACAACCTATACCTCCCGCTAACCCTCAACACACCCGCTCATATTAACCAGAAATGGT	420
lama.gua	CCGACAACCTATACCTCCCGCTAACCCTCAACACACCCGCTCATATTAACCAGAAATGGT	420
vic.vic	CCGACAACCTATACCCCGCTAACCCTCAACACACCCGCTCATATTAACCAGAAATGGT	420
cam.bac	CTGACAACCTATACCTCCCGCTAACCCTCAATACACCACCAACATTAAGCCGAAATGGT	420
arc.for	CAGACAACCTACACCCAGCAAAACCCCTCAGCACTCCACCACATATTAACCTGAATGGT	420
arc.gaz	CAGACAACCTACATCCAGCAAAACCCCTCAGTACTCCACCACATATCAAACCTGAATGGT	420
eum.jub	CAGACAACCTACATCCAGCAAAACCCCTCAGCACTCCACCACATATTAACCTGAATGGT	420
sal.cal	CAGACAACCTATATTCAGCAAAACCCCTCAGCACTCCACCACATATTAACCTGAATGGT	420
odo.ros	CCGACAATTACACCCAGCAAAACCCCTCAGCACTCCACCACATATCAAACCTGAATGGT	420
pho.fasciata	CCGACAACCTACACCCCTGCCAATCCCTAAGTACCCACCAACATATCAAAGCCGAAATGGT	420
pho.gro	CCGACAACCTACATCCCTGCCAATCCCTAAGTACCCACCAACATATCAAAGCCGAAATGGT	420
pho.vit	CCGACAACCTATATCCCTGCCAATCCCTAAGTACCCACCAACATATCAAAGCCGAAATGGT	420
cys.cri	CCGACAACCTATACCCCTGCCAATCCCTAAGTACCCACCAACATATTAACCTGAATGGT	420
hyd.lep	CCGACAACCTATATTCCTGCTAACCCTAAGTACCCACCAACATATCAAACCTGAATGGT	420
lep.wed	CCGACAACCTATACCTCCGCTAATCCCTAAGTACTCCACCACATATCAAACCTGAATGGT	420
mir.leo	CCGACAACCTACACCCCTGCCAATCCCTAAGTACCCACCAACATATTAAGCCGAAATGGT	420
eri.bar	CCGACAACCTACACTCCCTGCCAATCCCTAAGTACCCACCAACATATTAAGCCGAAATGGT	420
non.sch	CTGACAACCTACATCCCTGCCAATCCCTAAGTACCCACCAACATTAACCTGAATGGT	420
rel.mal	CTGACAACCTACATCCCTGCCAATCCCTAAGTACCCACCAACATTAACCTGAATGGT	420
rel.chi	CTGATAACTATACCCCGCAAAACCCACTGAGCACCCACCCACATCAAACCTGAATGGT	420
vil.ful	CTGATAACTATATTCCTGCTAACCCTAAGTACCCACCAACATTAACCTGAATGGT	420
lei	CAGACAACCTACATCCAGCAAAACCCCTTAATACCCCTCCCATATTAACCTGAATGGT	420
lan	CAGATAACTACACCCCTGCCAATCCCTAAGTACCCACCAACATTAACCTGAATGGT	420
al	CAGACAATTACATCCCGCAAAACCCCTAAGTACCCACCAACATTAACCTGAATGGT	420
la.sab	CAGACAACCTATACCCAGCAAAACCCACTAAGCACCCCTCCACATTAACCTGAATGGT	420
la.vol	CAGACAACCTATACCTCCAGCAAAACCCACTAAGCACCCCTCCCATATTAAGCCAGAAATGGT	420
yl.pha	CTGACAACCTACACCCCGCAAAACCCACTTAACACCCCTCCTCATATTAACCTGAATGGT	420

aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ore.ore	ATTTNCTATTNGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
add.nas	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ory.dam	ATTTTCTATTTCGCATATGCGATCCTTACGATCAATCCCCAATAAACTAGGAGG	472
hip.equ	ATTTTTTATTTCGCGTACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
alc.bus	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
sig.lic	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bea.hun	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
dam.lun	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
con.tau	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
amm.ler	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pse.nay	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.ibe	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
hem.jem	ATTTTCTATTTCGCATACGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.fal	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
rup.pyr	ATTTTCTATTTCGCATATGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
rup.rup	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
nem.cau	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bud.tax.tax	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pan.hod	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.amm	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.vig	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cap.cri	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ovi.mos	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ora.ame	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cep.dor	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cep.max	ATTTTCTATTTCGCGTACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bis.bon	ACTTCCTATTTCGCATANGCAATTTTACGGTCAATCCCCAATAAACTAGGAGG	472
bos.gru	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bos.tra	ATTTTCTGTTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
bub.min	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
buba.bub	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
tra.ang	ATTTTCTGTTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
tra.eur	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
kob.ell	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
kob.meg	ATTTTCTATTTCGCATACGCAATTTTACGGTCAATCCCCAATAAACTAGGAGG	472
red.aru	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
red.ful	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
neo.mos	ACTTTTTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pel.cap	ATTTTCTATTTCGCATATGCGATCCTACGATCAATCCCCAATAAACTAGGAGG	472
gas.dam	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
our.our	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ant.cer	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
sai.sai	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
mad.kir	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
rap.mel	ATTTTCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
gas.gas	ACTTCCTATTTCGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ant.ame	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
hyd.ine	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
mun.mun	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
alc.alc	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.ela.kan	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.ela.kan	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.ela.caa	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.nip.cenc	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.nip.yes	ACTTCCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
cer.nip.ker	ATTTTCTATTTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472

cer.nip.pul	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
cer.nip.nip	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
cer.ela.sco	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
cer.dam	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAATAAATAGGAGG	472
ran.tar	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAATAAATAGGAGG	472
mos.fus	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAACTAGGAGG	472
mos.leu	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAACTAGGAGG	472
mos.chr	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAACTAGGAGG	472
mos.ber	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAACTAGGAGG	472
mos.mos	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAATAGGAGG	472
tra.jav	ATTTCTATTTGCATACGCAATCTTCGGTCAATCCCAATAAATAGGAGG	472
trag.nap	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAATAGGAGG	472
bala.acu	ACTTCTATTTGCATACGCAATCCTACGATCAATCCCAATAAATAGGAGG	472
bala.bon	ATTTCTATTTGCATACGCAATCCTACGATCAATCCCAACAAATAGGAGG	472
bala.bor	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAATAGGAGG	472
bala.edi	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAATAGGAGG	472
esch.rob	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAATAGGAGG	472
bala.mus	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAATAGGAGG	472
mega.nov	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
bala.phy	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
cap.mar	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAATAGGAGG	472
ceph.com	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAATAAACTGGAGG	472
ceph.eut	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
lage.obl	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
ceph.heu	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
ceph.hec	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
lage.aus	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
lage.cru	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
lage.obs	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
lisso.bor	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
lisso.per	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
glo.mac	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAATAAACTGGAGG	472
glo.mel	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAATAAACTGGAGG	472
fere.att	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
pepo.ele	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAATAAACTGGAGG	472
gram.gri	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAATAAACTGGAGG	472
pse.cra	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCAACAAACTGGAGG	472
lage.acu	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAATAAACTGGAGG	472
orci.bre	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
orca.bre	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
del.cap	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
del.tro	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
del.del	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
sten.cly	ACTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
sten.coe	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
tur.adu	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
sten.fro	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
saus.chi	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
sten.lon	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
turs.tru	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTGGAGG	472
lage.alb	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTGGAGG	472
sten.bre	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCTAATAAACTGGAGG	472
sota.flu	ACTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
del.leu	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
mono.mon	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAACAAACTAGGAGG	472
plat.gan	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAATAAACTAGGAGG	472
plat.min	ATTTCTATTTGCATACGCAATCCTACGATCAATTTCCCAATAAACTAGGAGG	472
kogi.bre	ATTTCTATTTGCATATGCCATTCTACGATCAATTTCCCTAATAAACTAGGAGG	472

hyd.ine	CAGACAATTATACTCCAGCAAACCCACTCAATACACCCCCCTCACATTAACCCAGAATGAT	410
mun.mun	CCGACAATTATACCCAGCAAACCCACTCAATACACCCCCCTCACATCAAGCCTGAATGAT	420
alc.alc	CAGACAACCTACACCCAGCTAATCCACTCAACACACCCCCCTCATATTAAGCCTGAATGGT	410
cer.ela.kan	CAGACAACCTATACCCAGCAAATCCACTCAATACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.ela.xan	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.ela.can	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.nip.cent	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.nip.yes	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.nip.ker	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.nip.pul	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCACATTAACCCCTGAATGAT	420
cer.nip.nip	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
cer.ela.sco	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
cer.dam	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
ran.tar	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mos.fus	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mos.leu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mos.chr	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mos.ber	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mos.mos	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
tra.jav	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
trag.nap	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.acu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.bon	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.bor	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.edi	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
esch.rob	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.mus	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
mega.nov	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
bala.phy	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
cap.mar	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
ceph.com	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
ceph.eut	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lage.obl	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
ceph.heu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
ceph.hec	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lage.aus	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lage.cru	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lage.obs	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lisso.bor	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lisso.per	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
glo.mac	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
glo.mel	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
fere.att	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
pepo.ele	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
gram.gri	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
pse.cra	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
lage.acu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
orci.bre	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
orca.bre	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
del.cap	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
del.tro	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
del.del	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
sten.cly	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
sten.coe	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
tur.adu	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
sten.fro	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
aus.chi	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420
sten.lon	CAGACAACCTATACCCAGCAAATCCACTCAACACACCCCCCTCATATTAACCCCTGAATGAT	420

kogi.sim	ACTTTCTATTCCGCATACGCCATTCTACGATCAATTCCTAACAAACTGGGAGG	472
phys.cat	ATTTCCCTATTCCGCGTACGCCATCCTACGATCTGTCCCCAATAAACTAGGAGG	472
lipo.vex	ATTTCCCTATTCCGCATACGCCAATCTACGATCAATTCGCCAATAAACTAGGAGG	472
phoc.sin	ATTTCCCTATTCCGCATACGCCAATCTACGATCAATTCGCCAATAAACTAGGAGG	472
bera.bai	ACTTCCCTGTTCCGCATACGCCAATCTTACGATCAGTCCCTAATAAACTAGGGGG	472
ziph.car	ACTTCCCTATTCCGCATACGCCAATCTTACGATCAATTCGCCAATAAACTAGGAGG	472
meso.eur	ACTTCCCTATTCCGCATACGCCAATCTTACGATCAATTCGCCAATAAACTAGGAGG	472
meso.bid	ATTTCCCTATTCCGCATACGCCAATCTTACGATCAATTCGCCAATAAACTAGGAGG	472
meso.den	ATTTTCTATTTCGCATACGCCAATCTTACGATCAATTCGCCAATAAACTAGGAGG	472
hype.amp	ACTTCTTATTTCGCATACGCCAATCTTACGATCAATTCGCCAATAAACTAGGAGG	472
meso.per	ATTTTCTATTTCGCATATGCCAATTTTACGATCAGTTCCCTAATAAACTAGGAGG	472
pont.bla	ATTTCCCTATTTCGCCTACGCCATCCTACGATCAATTCGCCAATAAACTGGGAGG	472
hex.lib	ATTTCCCTGTTCCGCATACGCCAATCTCCGATCAATTCCTAACAATACTGGGAGG	472
hipp.amp	ATTTCCCTGTTCCGCGTACGCGATTCTCCGATCAATTCGCCAACAATACTAGGAGG	472
dic.sum	ACTTCCCTATTCCGCTACGCCAATCTTACGATCCATTCGCCAATAAACTAGGCGG	472
rhin.son	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
cera	ACTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
equu	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
baby.bab	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
phac.afr	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
sus.bar	ACTTCTTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
sus.scr.ewb3	ATTTCTTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
lama.gla	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
lama.gua	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
vic.vic	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
cam.bac	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGCGG	472
arc.for	ATTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
arc.gaz	ATTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
eum.jub	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
zal.cal	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
odo.ros	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pho.fasciata	ACTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pho.gro	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pho.vit	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
cys.cri	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
hyd.lep	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
lep.wed	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
mir.leo	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
eri.bar	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
mon.sch	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
hela.mal	ACTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
sel.chi	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
ail.ful	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
fel	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
can	ATTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
tal	ACTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
gla.sab	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
gla.vol	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
hyl.pha	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pet.set	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
bel.pea	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pte.mom	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
gala.demi	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
pero.pot	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
gala.mat	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
gala.moh	ACTTTTCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
oto.gar	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472
lor.tur	ATTTCCCTATTTCGCTTACGCCAATCTTACGATCCATTCGCCAACAATACTAGGAGG	472

PRIMER 'mc5869'

Results for RID 984593689-1224-27770



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770¹

Query-

(128 letters)

Database: Sequences from complete mitochondrial genomes
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reportsDistribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

(bits) Value

ref NC_001700.1	Felis catus mitochondrion, complete genome	365	e-101
ref NC_001325.1	Phoca vitulina mitochondrion, complete genome	198	1e-51
ref NC_002008.1	Canis familiaris mitochondrion, complete g...	190	4e-49
ref NC_001602.1	Halichoerus grypus mitochondrion, complete...	180	3e-46
ref NC_000884.1	Cavia porcellus complete mitochondrial genome	176	5e-45
ref NC_001808.1	Ceratotherium simum mitochondrion, complet...	155	2e-41
ref NC_001892.1	Myoxus glis mitochondrion, complete genome	151	8e-38
ref NC_001788.1	Equus asinus mitochondrion, complete genome	151	3e-37
ref NC_002073.1	Orycteropus afer complete mitochondrial ge...	149	1e-36
ref NC_001821.1	Dasyus novemcinctus mitochondrion, comple...	141	3e-34
ref NC_001779.1	R.unicornis complete mitochondrial genome	135	2e-32
ref NC_001569.1	Mus musculus mitochondrion, complete genome	133	7e-32
ref NC_000889.1	Hippopotamus amphibius mitochondrion, comp...	125	2e-29
ref NC_001640.1	Equus caballus mitochondrion, complete genome	125	2e-29
ref NC_001794.1	Macropus robustus mitochondrion, complete ...	123	7e-29
ref NC_000845.1	Sus scrofa mitochondrion, complete genome	121	3e-28
ref NC_001665.1	Rattus norvegicus mitochondrial genome	121	3e-28
ref NC_001567.1	Bos taurus mitochondrion, complete genome	121	3e-28
ref NC_001643.1	Pan troglodytes mitochondrion, complete ge...	117	4e-27
ref NC_001941.1	Ovis aries mitochondrion, complete genome	109	1e-24
ref NC_002391.1	Talpa europaea mitochondrion, complete genome	103	7e-23
ref NC_001913.1	Oryctolagus cuniculus mitochondrion, compl...	103	7e-23
ref NC_001644.1	Pan paniscus mitochondrion, complete genome	101	3e-22
ref NC_001807.2	Human mitochondrion, complete genome	99	4e-21
ref NC_001601.1	Balaenoptera musculus mitochondrion, compl...	98	4e-21
ref NC_002009.1	Artibeus jamaicensis mitochondrion, comple...	96	2e-20
ref NC_001645.1	Gorilla gorilla mitochondrion, complete ge...	92	2e-19
ref NC_001321.1	Balaenoptera physalus mitochondrion, compl...	90	1e-18
ref NC_001610.1	Didelphis virginiana mitochondrion, comple...	80	9e-16
ref NC_002082.1	Hylobates lar mitochondrion, complete genome	70	9e-13
ref NC_001727.1	Crossostoma lacustre mitochondrion, comple...	70	9e-13
ref NC_001804.1	Latimeria chalumnae mitochondrion, complet...	68	4e-12
ref NC_000880.1	Vidua chalybeata mitochondrion, complete g...	56	1e-11
ref NC_002069.1	Corvus frugilegus mitochondrion, complete ...	64	6e-11
ref NC_000886.1	Chelonia mydas mitochondrial DNA, complete...	62	2e-10
ref NC_001646.1	Pongo pygmaeus mitochondrion, complete genome	62	2e-10
ref NC_001606.1	Cyprinus carpio mitochondrion, complete ge...	62	2e-10
ref NC_000890.1	Mustelus manazo mitochondrion, complete ge...	60	9e-10
ref NC_001323.1	Gallus gallus mitochondrion, complete genome	60	9e-10
ref NC_002079.1	Carassius auratus mitochondrion, complete ...	58	3e-09
ref NC_000934.1	Loxodonta africana mitochondrion, complete...	56	1e-08
ref NC_000878.1	Falco peregrinus mitochondrion, complete g...	56	1e-08
ref NC_000846.1	Rhea americana mitochondrion, complete genome	56	1e-08
ref NC_002196.1	Ciconia boyciana mitochondrion, complete g...	54	5e-08
ref NC_001960.1	Salmo salar mitochondrion, complete genome	54	5e-08
ref NC_001778.1	Polypterus ornatipinnis mitochondrion, com...	54	5e-08
ref NC_002083.1	Pongo pygmaeus abelii mitochondrion, compl...	52	2e-07
ref NC_001953.1	Struthio camelus complete mitochondrial ge...	52	2e-07
ref NC_001947.1	Pelomedusa subrufa mitochondrion, complete...	52	2e-07
ref NC_001770.1	Arbacia lixula mitochondrion, complete genome	52	2e-07

Alignments

cmpseq_0	1	tgaatctgaggaggctctcagtagacaaagctacccgacacgattctcttgcctccac	60
NC_001700	15524g..g.....c.....a.....g.....	15583
NC_001325	15580a..t.....t.....a..t..a.....c.....	15639
NC_002008	14673c.....g.....a.....a.....t.....t.....	14729
NC_001602	15553a..t.....t.....a..t..a..g.....c.....	15612
NC_000884	14650g..g.....c.....a.....t.....t.....	14709
NC_001808	14662a..t..c..t.....c..a..c.....c.....t.....	14721
NC_001892	14654c.....c.....c.....t.....c.....c.....	14713
NC_001788	14671c..d.....c.....c.....c.....c.....c.....	14710
NC_002078	14663c.....c.....c.....a..a..a.....c.....	14716
NC_001821	14657c.....c.....c.....a..t..a.....c.....	14716
NC_001779	14664a.....c.....c.....c.....c.....c.....	14723
NC_001569	14625c.....g.....c.....c.....c.....c.....c.....	14684
NC_000889	14658c.....c.....c.....c.....c.....c.....	14717
NC_001640	14674c..a.....c.....c.....c.....c.....c.....	14711
NC_001794	14670g..a.....c.....c.....c.....c.....c.....	14727

[illegible]

tmpseq_0	61	ttcatcttccatttcatcttcagcttcagcagctccacctcttcttcttcacgag	120
NC_001700	15584t.....c.t.....ct.....g...a.....t.....t.....a	15643
NC_001325	15640a.....cg.ag.a.t.....a.....ac.....a.....a.....a	15699
NC_002008	14730c.t.c.c.....g.....at.....a.....t.a.....a.....a	14789
NC_001502	15613a.....cg.ag.a.t.....a.....a.....a.....a.....a	15672
NC_000884	14710	..t..t.....c.....a.c.c.....cgac.....t.....c.....	14769
NC_001808	14722	..t..t.c.c.....t.....at.c.....atcac.....a.....a	14781
NC_001892	14714	..t..t.a.c.c.t.tg.....c.....t.at.....c.....a	14773
NC_001788	14731	..t..t.a.c.....a.....c.g.t.atc.....t.a.....c.....a	14790
NC_002078	14717	..t..t.g.....t.tg.....tat.....t.....t.a.....a	14776
NC_001821	14717t.a.....t.....a.a.c.t.t.....gt.....a.....a	14776
NC_001779	14724	..t.....c.c.t.....ct.....c.....a.c.....a.....a	14783

NC	001569	14685c.a.....c...g.g.c.....atc..c.....c.....a	14744
NC	000889	14718	..t..c.....cg.c...a...a...cacc...t..a.....c..t..a	14777
NC	001640	14734a..c..c.....a...c.g.c..cc..a..t..a.....t.....a	14793
NC	001794	14730	..t.....a.....c.....a...c.....c.ct...t.....a.....	14789
NC	001794	14462a.....c.....a.....c.....c.....c.....a.....t.....g.....a	14475
NC	000845	15888	..t.....g.....c.....ta.c.c.c.....c..a..t.....g.....a	15947
NC	001665	14670c.....c..t...g.c.c.c..c...acc..a..t..t..t.....c.....a	14729
NC	001567	15060	..t.....c.....at...aa.c.cac.....a.....a.....a.....a	15119
NC	001643	14711	..t..t.a..c..c.....a...c..a..a..c..t..t.....c..a.....a	14770
NC	001941	14705	..t..cc.c.....c.....g.....c..c.cac..t.....a..c.....c.....a	14764
NC	002391	14731c.g.....c..cg.g..a...c.g...t.....gt.....c.....a	14790
NC	001913	14721c.g.....c.....c.....c.....c.....c.....c.....a.....a	14740
NC	001644	14712	..t.....a..c..c..c..t..a...c.....a..a..c..t..t.....c.....a	14771
NC	001807	15293c.g..c..c..c..t..cg.....c.....c.....a..c.....c.g.....a	15352
NC	001601	15156c..c..c..c..c..cat...at...acc.....a..c.....c.....a	15215
NC	002009	14596	..tc.a.....c..c..cg..aa.....t..at.....cc.....t..a.....a	14755
NC	001645	14715	..t.....a..c..c.....a...c..a..a..cc.....c.....c..a.....a	14774
NC	001321	15159	..t.....c..c..c.....c..t..at...atc.....ca..t.....c.....a	15218
NC	001610	14723	..c..c.....c.....c..t..c..a..t..t..a..t..t.....c.....a	14782
NC	002085	14713a..c..c..c..a.g..c.....cc.g.....t.....a.....a	14772
NC	001727	15824a.....c.....c.....c.....c.....c.....c.....c.....a	15826
NC	001727	15872a.....c.....c.....c.....c.....c.....c.....c.....a	15843
NC	001804	14887c.....g.....c.....c.....c.....c.....c.....c.....a	14902

NC_001804	14928g..c.....t...	14948
NC_000880	15567ac.....a.....a	15591
NC_002069	14244	...c...a..c...g..a...g...gc...a..ct...t.....aacc.....a	14303
NC_000886	14778	...	14780
NC_001646	14737a..a..t..c.....ta.....a..a..cc..t.....a	14796
NC_001606	15839	...	15841
NC_000890	14901	..	14902
NC_002079	15842	...c....a.....	15862
NC_000934	14693t.....	14708
NC_000878	14264	...c.a.....	14277
NC_000846	14235a.....a	14246
NC_000846	14187	...	14189
NC_001960	15930	...	15932
NC_001778	14823t.....	14833
NC_001953	14170	...c....c.....	14184
NC_001770	15120	...	15122

tmpseq_0	121	acaggatctaacaccccccaggaatagtatccgactcagacaaaattccattccaccca	180
NC_001700	15644tac.....t.....c.....	15703
NC_001325	15700a.....c.....ca.....c.....g	15759
NC_002008	14790	..c....c.....t.....cac...a.....c.....t	14849
NC_001602	15673a.....c.....ca..c.....c.....g	15732
NC_000884	14770a.....a.....c..aac..a....c.....c.....t	14829
NC_001808	14782c..t....a.....ccc...a..at.....c.....t	14841
NC_001892	14774g..t....a.....t..aac..a..a.....c.....g	14833
NC_001788	14791c.....ccc...t..at.....c.....t	14850
NC_002078	14777t..t....t..t....t..a..t.....c..t.....t	14836
NC_001821	14777a.....a.....t..ctcg..aa..at....c..c.....g	14836
NC_001779	14784g..c.....a.....tcc...a..at.....c.....t	14843
NC_001569	14745a.....aa.....t..aac..a..tg....t.....c.....c	14804
NC_000889	14778c.....aa.....cccc..aa..g.....c.....t	14837
NC_001640	14794t.....ccc.....tatg.....c.....t	14853
NC_001794	14790	..c..t....a..t....caacc.....c.....t	14849
NC_000845	15948	..c....c.....ta..c....ctc...a..at.....t.....c	16007
NC_001665	14730a..t....a.....t..aac.....g.....c.....t	14789
NC_001567	15120c..c.....aa.....tccc..a..gt.....c.....c	15179
NC_001643	14771a..t....ct....cacc...c....c.....a..c.....c	14830
NC_001941	14765c.....a.....tcc...g..a....t.....c.....c	14824
NC_002391	14791a.....a.....	14814
NC_001913	14815t.....c.....c.....c	14840
NC_001644	14772a..t....ct....cacc...c....c.....a..c.....c	14811
NC_001807	15353	..g....a.....ct....cacc...c..t..c..t....ca..c.....t	15412
NC_001601	15216c.....a.....ccc...t..at...t.....c.....c	15275
NC_002009	14756a.....c..tcc...a..c.....t.....c.....c	14815
NC_001645	14775a.....tcc...c..cccc...c....t.....ca..c.....c	14834
NC_001321	15219c.....a.....c..ccc.....at...t.....c.....c	15278
NC_001610	14783a..g...t..aa....cc...a.....t.....c.....c	14842

NC_002082	14773a.....t....t....c..ctcc...c..ac.....cg..c.....c	14832
NC_001727	15884c..c.....g...cc..aac.....g.....t....ct..c.....	15943
NC_001804	14949c.....	14965
NC_000880	15592a.....t..aac.....tcc...a....gt.....c.....c	15651
NC_002069	14304c..a.....gct...c..tccc...a....gc.....c.....c	14363
NC_001646	14797a..t....	14814
NC_001323	15531t.....c.....c.....	15561
NC_002079	15939t..t.....	15961
NC_000934	14786c..c..t.....	14812
NC_000878	14363c.....	14383
NC_000846	14247	..c..g..c.....t.....c.....tcc...t.....c.....c	14306
NC_002196	16371c.....	16391
NC_002083	14858c..c.....	14866
NC_001953	14269c..c.....	14289

tmpseq_0	181	cactacacacatcaaaagatattccggggcctctcagtaactaactcagcactcactactc	240
NC_001700	15704c.....c.....a..t.....g..tc...a.....	15763
NC_001325	15760c.....c.....a..gggc...c..c..t....tc...a..c.....	15817
NC_002079	14850g.....	14972
NC_001602	15733c.....c.....	15755
NC_001602	15786a.....	15772

NC_000884	14810	..t.....	14846
NC_001808	14842c.....aa..t..c.c.....ac.cgcc..a	14901
NC_001892	14834	..t.....t.....c..a.....a..cc....c..tt.cccc.....acc..a	14893
NC_001788	14851c.....c.....a..a.....	14882
NC_001788	15080		15095
NC_002078	14837	14853
NC_001821	14837t.....t.....	14859
NC_001779	14844c.....	14866
NC_001569	14805t.....	14827
NC_000889	14838	..t.....g..c.....	14860
NC_001640	14854	..t..t.....t.....c.....	14876
NC_001640	15085		15098
NC_001794	14850	..t..t..t.....	14867
NC_000845	16008t.....t.....	16024
NC_001665	14790	..t..t.....t.....	14806
NC_001567	15180c..c..t..g..c..t.....c.....t.....t..a.....a	15219

ag

NC_001643	14831	14853
NC_001941	14825	..t.....c..t.....c.....	14847
NC_001913	14841	14857
NC_001644	14832c.....	14854
NC_001807	15413	15429
NC_001601	15276t.....	15292
NC_002009	14816t..t..t.....	14835
NC_001645	14835c.....c.....a.....	14863
NC_001321	15279	..c.....t.....	15295
NC_001610	14843t..c..a.....	14865
NC_002082	14833t.....c.....	14855
NC_001727	15944	15947
NC_000880	15652	15659
NC_002069	14364t.....	14381
NC_001323	15562t..ct.....c..t.....	15588
NC_002079	15962	15965
NC_000934	14813	14817
NC_000878	14384t..tc.....	14406
NC_000846	14307	14310
NC_002196	16392t..t..cc.....a.....	16421
NC_002083	14867c.....a.....	14895
NC_001953	14290	14293

cmpseq_0	241	gtccattatccaccagacctgttaggagaccocgataaactacatccctcgccaaacctccca	300
NC_001700	15764t.....c.....a..c.....a.....t..	15823
NC_001325	15820	..g.....c.....a..c.....t.....	15867
NC_002008	14914t.....c.....a.....a.....c.....a.....c...	14969
NC_001602	15793	..a.....c.....a..g.....c.....t..c...	15852
NC_000884	14900c.....a.....a.....ca..c.....g..g	14949
NC_001808	14902	..t.....a..cc.....t..c.....c.....t.....	14960
NC_001892	14894	..t.....c.....t..a.....c.....c.....a...	14953
NC_002078	14909a.....	14928
NC_000845	16071ac.....a..c.....c.....a..a.....a...	16127
NC_001567	15240	..a.....g..c.....cc..c.....a.....c.....a.....	15272
NC_001913	14901t.....a.....a..c.....c.....c.....c..t	14950
NC_001644	1484		1492
NC_001807	15476cc.....c.....a..c..t..t..c..ca.....ct..	15932
NC_002009	14880t.....cc.....a..c..t..t..t..a..a..t..a..t	14935
NC_001645	14898cc.....a..c.....c..ta.....c.....	14954
NC_001610	14907t..t.....t..c..t..c..a..t..t..c..t	14962
NC_002082	14950		14952
NC_001804	15071a..t..a.....a.....	15108
NC_000886	14980a..c.....t..ca..a.....	15017
NC_002196	16454ca.....ac.....t.....a..g..t..c.....a.....	16307
NC_001950	16155		16169

cmpseq_0	301	aatcccccccccatatccaagccctgaat	328
NC_001700	15824t..a.....	15871
NC_002008	14970	..c.....a.....t.....	14975
NC_001602	15833	..gc.....a.....	15872
NC_000884	14950		14954
NC_001892	14754	..g.....	14770

63

NC 001779	3081	3094
NC 000845	16128	..c.....a.....	16144
NC 001911	14961	14980
NC 001644	1493	...c.....	1501
NC 001807	15533	..c.....c.....c....	15560
NC 002009	14936c.....a....	14963
NC 001645	14955	.gc.....a.....c....	14974
NC 001610	14963	..c.....g..c.....a....	14990
NC 002082	14953	..c.....c.....	14972
NC 001960	16170	gt...t..a..t.....	16197
NC 001951	14426c....	14437

Database: Sequences from complete mitochondrial genomes

Posted date: Jun 28, 2000 10:56 AM

Number of letters in database: 3,164,247

Number of sequences in database: 129

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 788
 Number of Sequences: 129
 Number of extensions: 788
 Number of successful extensions: 168
 Number of sequences better than 10.0: 77
 length of query: 328
 length of database: 3,164,247
 effective HSP length: 15
 effective length of query: 313
 effective length of database: 3,162,312
 effective search space: 989803656
 effective search space used: 989803656
 T: 0
 A: 30
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 14 (28.2 bits)

Table 4



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query-

(328 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

	Score (bits)	E Value
gb AY005809.1 Panthera pardus cytochrome b gene, partial c...	603	e-170
gb AF051054.1 AF051054 Panthera tigris sumatrae isolate Su1...	527	e-147
gb AF051053.1 AF051053 Panthera tigris tigris isolate 87 mi...	527	e-147
gb AF051050.1 AF051050 Panthera tigris corbetti isolate C2 ...	476	e-132
gb AF051049.1 AF051049 Panthera tigris corbetti isolate C1 ...	476	e-132
gb AF051025.1 AF051025 Panthera tigris tigris isolate 89 cy...	460	e-127
gb AF051024.1 AF051024 Panthera tigris tigris isolate 88 cy...	460	e-127
gb AF051023.1 AF051023 Panthera tigris tigris isolate 87 cy...	460	e-127
gb AF051022.1 AF051022 Panthera tigris tigris isolate 86 cy...	460	e-127
gb AF051021.1 AF051021 Panthera tigris tigris isolate 85 cy...	460	e-127
gb AF051018.1 AF051018 Panthera tigris tigris isolate 82 cy...	460	e-127
gb AF051051.1 AF051051 Panthera tigris corbetti isolate C3 ...	452	e-125
gb AF051048.1 AF051048 Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051047.1 AF051047 Panthera tigris sumatrae isolate Su9...	452	e-125
gb AF051046.1 AF051046 Panthera tigris sumatrae isolate Su7...	452	e-125
gb AF051045.1 AF051045 Panthera tigris sumatrae isolate Su6...	452	e-125
gb AF051044.1 AF051044 Panthera tigris sumatrae isolate Su5...	452	e-125
gb AF051042.1 AF051042 Panthera tigris sumatrae isolate Su3...	452	e-125
gb AF051041.1 AF051041 Panthera tigris sumatrae isolate Su2...	452	e-125
gb AF051040.1 AF051040 Panthera tigris sumatrae isolate Su1...	452	e-125
gb AF051039.1 AF051039 Panthera tigris altaica isolate S15 ...	452	e-125
gb AF051038.1 AF051038 Panthera tigris altaica isolate S14 ...	452	e-125
gb AF051037.1 AF051037 Panthera tigris altaica isolate S13 ...	452	e-125
gb AF051036.1 AF051036 Panthera tigris altaica isolate S12 ...	452	e-125
gb AF051035.1 AF051035 Panthera tigris altaica isolate S11 ...	452	e-125
gb AF051034.1 AF051034 Panthera tigris altaica isolate S10 ...	452	e-125
gb AF051033.1 AF051033 Panthera tigris altaica isolate S8 c...	452	e-125
gb AF051032.1 AF051032 Panthera tigris altaica isolate S7 c...	452	e-125
gb AF051031.1 AF051031 Panthera tigris altaica isolate S6 c...	452	e-125
gb AF051030.1 AF051030 Panthera tigris altaica isolate S5 c...	452	e-125
gb AF051029.1 AF051029 Panthera tigris altaica isolate S4 c...	452	e-125
gb AF051028.1 AF051028 Panthera tigris altaica isolate S3 c...	452	e-125
gb AF051027.1 AF051027 Panthera tigris altaica isolate S2 c...	452	e-125
gb AF051026.1 AF051026 Panthera tigris altaica isolate S1 c...	452	e-125
gb AF051020.1 AF051020 Panthera tigris tigris isolate 84 cy...	452	e-125
gb AF051019.1 AF051019 Panthera tigris tigris isolate 83 cy...	444	e-122
gb AF051043.1 AF051043 Panthera tigris sumatrae isolate Su4...	444	e-122
emb X82301.1 MIPTCTB P.tigris mitochondrial cytochrome b gene	440	e-121
gb AF051052.1 AF051052 Panthera leo cytochrome b (cytb) gen...	438	e-121
emb X82300.1 MIPLCTB P.leo mitochondrial cytochrome b gene	399	e-106
gb AB004238.1 AB004238 Felis catus mitochondrial DNA for c...	381	e-103
gb AB004237.1 AB004237 Felis catus mitochondrial DNA for c...	377	e-102
emb X82296.1 MIFDCTB F.domesticus mitochondrial cytochrome...	365	1e-98
gb NC 001700.1 Felis catus mitochondrion, complete genome	363	1e-98
gb U20753.1 FCU20753 Felis catus mitochondrion, complete ge...	276	7e-72
gb AF125145.1 AF125145 Viverricula indica cytochrome b gene...	270	4e-70
gb AF125144.1 AF125144 Chrotogale owstoni cytochrome b gene...	255	7e-66
gb AF154975.1 AF154975 Martes martes specimen voucher AF175...	255	7e-66
gb AB051237.1 AB051237 Martes martes mitochondrial cytb ge...	246	6e-63
gb AF125149.1 AF125149 Viverra zibetha cytochrome b gene...		

Alignments

cmpseq_0	1	tgaatctgaggaggctcttcagtagacaaagctaccctgacacgattctcttgcctccac	60
AY005809	39g.....c.....	98
AF051054	487g.....c.....	546
AF051053	487g.....c.....	546
AF051050	487g.....c.....	546
AF051049	487g.....c.....	546
AF051025	487g.....c.....	546
AF051024	487g.....c.....	546
AF051023	487g.....c.....	546
AF051022	487g.....c.....	546
AF051021	487g.....c.....	546
AF051018	487g.....c.....	546
AF051051	487g.....c.....	546
AF051048	487g.....c.....	546
AF051047	487g.....c.....	546

AF053046	487g..t.....	546
AF053045	487g..t.....	546
AF053044	487g..t.....	546
AF053042	487g..t.....	546
AF053041	487g..t.....	546
AF053040	487g..t.....	546
AF053039	487g..t.....	546
AF053038	487g..t.....	546
AF053037	487g..t.....	546
AF053036	487g..t.....	546
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AF053031	487g..t.....	546
AF053030	487g..t.....	546
AF053029	487g..t.....	546
AF053028	487g..t.....	546
AF053027	487g..t.....	546
AF053026	487g..t.....	546
AF053020	487g..t.....	546
AF053019	487g..t.....	546
AF053043	487g..t.....	546
X82301	487g..t.....	546
AF053052	487c.....	546
X82300	490c.....	546
AB004238	487g.....c.....a.....	546
AB004237	487g.....c.....a.....	546
X82296	487g.....c.....a.....	546
NC 001700	15524g..g.....c.....a.....g.....	15583
U20753	15524g..g.....c.....a.....g.....	15583
AF125145	357t.....c..t.a..c.....c.....	416
AF125144	357t.....g.....t.....t.....c.....a.....c.....	416
AF154975	487g.....g.....c.....a..g.....c.....	546
AB051237	487g.....g.....c.....a..g.....c.....	546
AF125149	357g.....t.....g.....c.....t.a.....t.....	416
cmpseq_0	61	ttcatccttccatttatcatctcagctctagcagcagtcacccctctattccttcacgag	120
AX005809	99	153
AF053054	547c.....c..t.....	606
AF053053	547c.....c..t.....	606
AF053050	547g.....c.....a	606
AF053049	547g.....c.....a	606
AF053025	547g.....g.....c.....a	606
AF053024	547g.....g.....c.....a	606
AF053023	547g.....g.....c.....a	606
AF053022	547g.....g.....c.....a	606
AF053021	547g.....g.....c.....a	606
AF053018	547g.....g.....c.....a	606
AF053051	547g.....g.....c.....a	606
AF053048	547g.....g.....c.....a	606
AF053047	547g.....g.....c.....a	606
AF053046	547g.....g.....c.....a	606
AF053045	547g.....g.....c.....a	606
AF053044	547g.....g.....c.....a	606
AF053043	547g.....g.....c.....a	606
AF053041	547g.....g.....c.....a	606
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AF053031	547g.....g.....c.....a	606
AF053030	547g.....g.....c.....a	606
AF053029	547g.....g.....c.....a	606
AF053028	547g.....g.....c.....a	606
AF053027	547g.....g.....c.....a	606

AF051026	547g.....g.....c.....a	606
AF051020	547g.....g.....c.....a	606
AF051019	547g.....g.....c.....a	606
AF051043	547c.....g.....g.....c.....a	606
X82101	547c.....g.....g.....c.....a	606
AF051052	547g.....g.....c.....a	606
X82100	547g.....g.....c.....a	606
AB004238	547c.....c.....c.....a	606
AB004237	547c.....c.....c.....a	606
X82296	547c.....c.....c.....a	606
NC 001700	15584c.....c.....c.....g.....a.....c.....a	15643
U20753	15584c.....c.....c.....g.....a.....c.....a	15643
AF125145	417c.....c.....c.....c.....a.....a.....a	476
AF125144	417c.....c.....c.....c.....a.....a.....a	476
AF154975	547g.....c.....c.....a.....c.....c.....a	606
AB051237	547g.....c.....c.....a.....c.....c.....a	606
AF125149	417c.....c.....c.....c.....a.....a.....a	476
cmpseq_0	121	acaggatcctaacaacccctcaggaatagtatccgactcagacaaaattccattccaccca	180
AY005809	159c.....c.....c.....c.....c.....c.....c	218
AF053054	607c.....c.....c.....c.....c.....c.....c	666
AF053053	607c.....c.....c.....c.....c.....c.....c	666
AF053050	607c.....c.....c.....c.....c.....c.....c	666
AF053049	607c.....c.....c.....c.....c.....c.....c	666
AF053025	607c.....c.....c.....c.....c.....c.....c	666
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AF053023	607c.....c.....c.....c.....c.....c.....c	666
AF053022	607c.....c.....c.....c.....c.....c.....c	666
AF053021	607c.....c.....c.....c.....c.....c.....c	666
AF053019	607c.....c.....c.....c.....c.....c.....c	666
AF053051	607c.....c.....c.....c.....c.....c.....c	666
AF053048	607c.....c.....c.....c.....c.....c.....c	666
AF053047	607c.....c.....c.....c.....c.....c.....c	666
AF053046	607c.....c.....c.....c.....c.....c.....c	666
AF053045	607c.....c.....c.....c.....c.....c.....c	666
AF053044	607c.....c.....c.....c.....c.....c.....c	666
AF053042	607c.....c.....c.....c.....c.....c.....c	666
AF053041	607c.....c.....c.....c.....c.....c.....c	666
AF053040	607c.....c.....c.....c.....c.....c.....c	666
AF053039	607c.....c.....c.....c.....c.....c.....c	666
AF053038	607c.....c.....c.....c.....c.....c.....c	666
AF053037	607c.....c.....c.....c.....c.....c.....c	666
AF053036	607c.....c.....c.....c.....c.....c.....c	666
AF053035	607c.....c.....c.....c.....c.....c.....c	666
AF053034	607c.....c.....c.....c.....c.....c.....c	666
AF053033	607c.....c.....c.....c.....c.....c.....c	666
AF053032	607c.....c.....c.....c.....c.....c.....c	666
AF053031	607c.....c.....c.....c.....c.....c.....c	666
AF053030	607c.....c.....c.....c.....c.....c.....c	666
AF053029	607c.....c.....c.....c.....c.....c.....c	666
AF053028	607c.....c.....c.....c.....c.....c.....c	666
AF053027	607c.....c.....c.....c.....c.....c.....c	666
AF053026	607c.....c.....c.....c.....c.....c.....c	666
AF053020	607c.....c.....c.....c.....c.....c.....c	666
AF053019	607c.....c.....c.....c.....c.....c.....c	666
AF053043	607c.....c.....c.....c.....c.....c.....c	666
X82101	607c.....c.....c.....c.....c.....c.....c	666
AF051052	607c.....c.....c.....c.....c.....c.....c	666
X82100	607c.....c.....c.....c.....c.....c.....c	666
AB004238	607c.....c.....c.....c.....c.....c.....c	666
AB004237	607c.....c.....c.....c.....c.....c.....c	666
X82296	607c.....c.....c.....c.....c.....c.....c	15703
NC 001700	15644c.....c.....c.....c.....c.....c.....c	15703
U20753	15644c.....c.....c.....c.....c.....c.....c	536
AF125145	477c.....c.....c.....c.....c.....c.....c	536
AF125144	477c.....c.....c.....c.....c.....c.....c	666
AF154975	607c.....c.....c.....c.....c.....c.....c	666
AB051237	607c.....c.....c.....c.....c.....c.....c	666
AF125142	477c.....c.....c.....c.....c.....c.....c	536
cmpseq_0	181	cactccacacacccaaagatctctggtggtctctagtcactaatctcagcactcactcctc	240

AY005809	219c.....	278
AF053054	667c.....a.....	726
AF053053	667c.....a.....	726
AF053050	667c.....a.....c.....	726
AF053049	667c.....a.....c.....	726
AF053029	667c.....a.....c.....	726
AF053024	667c.....a.....c.....	726
AF053023	667c.....a.....c.....	726
AF053022	667c.....a.....c.....	726
AF053021	667c.....a.....c.....c.....	726
AF053018	667c.....a.....c.....c.....	726
AF053051	667c.....a.....c.....g.....a.....c.....	726
AF053048	667c.....a.....c.....g.....a.....c.....	726
AF053047	667c.....a.....c.....g.....a.....c.....	726
AF053046	667c.....a.....c.....g.....a.....c.....	726
AF053045	667c.....a.....c.....g.....a.....c.....	726
AF053044	667c.....a.....c.....g.....a.....c.....	726
AF053042	667c.....a.....c.....g.....a.....c.....	726
AF053041	667c.....a.....c.....g.....a.....c.....	726
AF053040	667c.....a.....c.....g.....a.....c.....	726
AF053039	667c.....a.....c.....a.....c.....c.....	726
AF053038	667c.....a.....c.....a.....c.....c.....	726
AF053037	667c.....a.....c.....a.....c.....c.....	726
AF053036	667c.....a.....c.....a.....c.....c.....	726
AF053035	667c.....a.....c.....a.....c.....c.....	726
AF053034	667c.....a.....c.....a.....c.....c.....	726
AF053033	667c.....a.....c.....a.....c.....c.....	726
AF053032	667c.....a.....c.....a.....c.....c.....	726
AF053031	667c.....a.....c.....a.....c.....c.....	726
AF053030	667c.....a.....c.....a.....c.....c.....	726
AF053029	667c.....a.....c.....a.....c.....c.....	726
AF053028	667c.....a.....c.....a.....c.....c.....	726
AF053027	667c.....a.....c.....a.....c.....c.....	726
AF053026	667c.....a.....c.....a.....c.....c.....	726
AF053020	667c.....a.....c.....a.....c.....c.....	726
AF053019	667c.....a.....c.....g.....a.....c.....	726
AF053043	667c.....a.....c.....g.....a.....c.....	726
X82301	667c.....a.....c.....g.....a.....c.....	726
AF053052	667c.....a.....c.....c.....a.....	726
X82300	667c.....a.....c.....c.....a.....	726
AB004238	667c.....a.....c.....g.....c.....a.....	726
AB004237	667c.....a.....c.....g.....c.....a.....	726
X82296	667c.....a.....c.....g.....c.....a.....	15763
NC 001700	15704c.....a.....c.....g.....c.....a.....	15763
U20753	15704c.....a.....c.....g.....c.....a.....	596
AF125145	537c.....a.....c.....c.....c.....a.....c.....g.....a.....	596
AF125144	537c.....a.....c.....c.....c.....a.....c.....g.....a.....	726
AF154975	667c.....a.....g.....c.....c.....c.....g.....a.....a.....	726
AB051237	667c.....a.....g.....c.....c.....c.....g.....a.....a.....	596
AF125149	537c.....a.....c.....c.....c.....c.....c.....a.....g.....a.....	596
cmpseq_0	241	gccccattctccaccagacctgctaggagaccctgataaactacatccctgccaaccctcta	100
AY005809	279c.....	338
AF053054	727a.....g.....c.....	786
AF053053	727a.....g.....c.....	786
AF053050	727a.....c.....c.....	786
AF053049	727a.....c.....c.....	786
AF053029	727a.....c.....c.....	786
AF053024	727a.....c.....c.....	786
AF053023	727a.....c.....c.....	786
AF053022	727a.....c.....c.....	786
AF053021	727a.....c.....c.....	786
AF053018	727a.....c.....c.....	786
AF053051	727a.....c.....c.....	786
AF053048	727a.....c.....c.....	786
AF053047	727a.....c.....c.....	786
AF053046	727a.....c.....c.....	786
AF053045	727a.....c.....c.....	786
AF053044	727a.....c.....c.....	786
AF053043	727a.....c.....c.....	786
AF053042	727a.....c.....c.....	786
AF053041	727a.....c.....c.....	786
AF053040	727a.....c.....c.....	786
AF053039	727a.....c.....c.....	786
AF053038	727a.....c.....c.....	786
AF053037	727a.....c.....c.....	786
AF053036	727a.....c.....c.....	786
AF053035	727a.....c.....c.....	786
AF053034	727a.....c.....c.....	786
AF053033	727a.....c.....c.....	786
AF053032	727a.....c.....c.....	786
AF053031	727a.....c.....c.....	786
AF053030	727a.....c.....c.....	786
AF053029	727a.....c.....c.....	786
AF053028	727a.....c.....c.....	786
AF053027	727a.....c.....c.....	786
AF053026	727a.....c.....c.....	786
AF053020	727a.....c.....c.....	786
AF053019	727a.....c.....c.....	786
AF053043	727a.....c.....c.....	786
AF053052	727a.....c.....c.....	786
X82301	727a.....c.....c.....	786
X82300	727a.....c.....c.....	786
AB004238	727a.....c.....c.....	786
AB004237	727a.....c.....c.....	786
X82296	727a.....c.....c.....	786
NC 001700	727a.....c.....c.....	786
U20753	727a.....c.....c.....	786
AF125145	727a.....c.....c.....	786
AF125144	727a.....c.....c.....	786
AF154975	727a.....c.....c.....	786
AB051237	727a.....c.....c.....	786
AF125149	727a.....c.....c.....	786

<u>AF053040</u>	727a.....c.....	786
<u>AF053039</u>	727a.....c.....c.....c.....	786
<u>AF053038</u>	727a.....c.....c.....c.....	786
<u>AF053037</u>	727a.....c.....c.....c.....	786
<u>AF053036</u>	727a.....c.....c.....c.....	786
<u>AF053035</u>	727a.....c.....c.....c.....	786
<u>AF053034</u>	727a.....c.....c.....c.....	786
<u>AF053033</u>	727a.....c.....c.....c.....	786
<u>AF053032</u>	727a.....c.....c.....c.....	786
<u>AF053031</u>	727a.....c.....c.....c.....	786
<u>AF053030</u>	727a.....c.....c.....c.....	786
<u>AF053029</u>	727a.....c.....c.....c.....	786
<u>AF053028</u>	727a.....c.....c.....c.....	786
<u>AF053027</u>	727a.....c.....c.....c.....	786
<u>AF053026</u>	727a.....c.....c.....c.....	786
<u>AF053020</u>	727a.....c.....c.....c.....	786
<u>AF053019</u>	727a.....c.....c.....c.....	786
<u>AF053043</u>	727a.....c.....c.....c.....	786
<u>X82301</u>	727a.....c.....c.....c.....	786
<u>AF053052</u>	727a.....c.....c.....c.....c.....c.....	786
<u>X82300</u>	727a.....c.....c.....c.....c.....	786
<u>AB004238</u>	727c.....c.....a.....c.....g.....a.....c.....	786
<u>AB004237</u>	727c.....c.....c.....a.....c.....a.....c.....	786
<u>X82296</u>	727c.....c.....c.....a.....c.....a.....c.....	786
<u>NC 001700</u>	15764c.....c.....a.....c.....a.....c.....	15823
<u>U20753</u>	15764c.....c.....a.....c.....a.....c.....	15823
<u>AF125145</u>	597c.....c.....a.....c.....c.....c.....	650
<u>AF125144</u>	597	..c.....c.....c.....a.....c.....c.....a.....	656
<u>AF154975</u>	727	..a.....c.....c.....g.....a.....c.....c.....a.....c.....	786
<u>AB051237</u>	727	..a.....c.....c.....g.....a.....c.....c.....a.....c.....	786
<u>AF125149</u>	597c.....c.....a.....c.....c.....c.....	656
<u>cmpseq_0</u>	301	aatacccccccccatataagccggaac	329
<u>AY005809</u>	339	366
<u>AF053054</u>	787	..c.....	808
<u>AF053053</u>	787	..c.....	808
<u>AF053050</u>	787c.....c.....	814
<u>AF053049</u>	787c.....c.....	814
<u>AF053025</u>	787c.....c.....	814
<u>AF053024</u>	787c.....c.....	814
<u>AF053023</u>	787c.....c.....	814
<u>AF053022</u>	787c.....c.....	814
<u>AF053021</u>	787c.....c.....	814
<u>AF053018</u>	787c.....c.....	814
<u>AF053051</u>	787c.....c.....	814
<u>AF053048</u>	787c.....c.....	814
<u>AF053047</u>	787c.....c.....	814
<u>AF053046</u>	787c.....c.....	814
<u>AF053045</u>	787c.....c.....	814
<u>AF053044</u>	787c.....c.....	814
<u>AF053042</u>	787c.....c.....	814
<u>AF053041</u>	787c.....c.....	814
<u>AF053040</u>	787c.....c.....	814
<u>AF053039</u>	787c.....c.....	814
<u>AF053038</u>	787c.....c.....	814
<u>AF053037</u>	787c.....c.....	814
<u>AF053036</u>	787c.....c.....	814
<u>AF053035</u>	787c.....c.....	814
<u>AF053034</u>	787c.....c.....	814
<u>AF053033</u>	787c.....c.....	814
<u>AF053032</u>	787c.....c.....	814
<u>AF053031</u>	787c.....c.....	814
<u>AF053030</u>	787c.....c.....	814
<u>AF053029</u>	787c.....c.....	814
<u>AF053028</u>	787c.....c.....	814
<u>AF053027</u>	787c.....c.....	814
<u>AF053026</u>	787c.....c.....	814
<u>AF053020</u>	787c.....c.....	814
<u>AF053019</u>	787c.....c.....	814
<u>AF053043</u>	787c.....c.....	814
<u>X82301</u>	787c.....c.....	814

<u>AF051052</u>	787	.gc.....a.....	812
<u>X82100</u>	787	.gc.....a.....	814
<u>AB004238</u>	787c..a.....	814
<u>AB004237</u>	787c..a.....	814
<u>X82296</u>	787c..a.....	814
<u>NC 001700</u>	15824c..a.....	15851
<u>U20753</u>	15824c..a.....	15851
<u>AF125144</u>	657	..c.....	664
<u>AF154975</u>	787	..c..a..a.....	803
<u>AB051237</u>	787	..c..a..a.....	803
<u>AF125149</u>	657	..c.....	664

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,861,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 460542

Number of Sequences: 807597

Number of extensions: 460542

Number of successful extensions: 22671

Number of sequences better than 10.0: 6487

length of query: 328

length of database: 2,861,827,885

effective HSP length: 20

effective length of query: 308

effective length of database: 2,847,675,945

effective search space: 877084191060

effective search space used: 877084191060

T: 0

A: 10

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 19 (38.2 bits)

Table 5. Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	<i>Panthera tigris tigris</i>
2	bhz26t	Indian tiger	<i>Panthera tigris tigris</i>
3	bhz30t	Indian tiger	<i>Panthera tigris tigris</i>
4	bhz45t	Indian tiger	<i>Panthera tigris tigris</i>
5	bhz56t	Indian tiger	<i>Panthera tigris tigris</i>
6	bhz63t	Indian tiger	<i>Panthera tigris tigris</i>
7	bhz20wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
8	bhz22wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
9	bhz23wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
10	bhz28wt	Indian white tiger	<i>Panthera tigris bengalensis</i>
11	gz1l	Normal leopard	<i>Panthera pardus</i>
12	gz2l	Normal leopard	<i>Panthera pardus</i>
13	gz3l	Normal leopard	<i>Panthera pardus</i>
14	gz21cl	Clouded leopard	<i>Neofelis nebulosa</i>
15	gz22cl	Clouded leopard	<i>Neofelis nebulosa</i>
16	darz14sl	Snow leopard	<i>Panthera uncia</i>
17	darz15sl	Snow leopard	<i>Panthera uncia</i>
18	darz16sl	Snow leopard	<i>Panthera uncia</i>
19	sbz22al	Asiatic lion	<i>Panthera leo persica</i>
20	sbz38al	Asiatic lion	<i>Panthera leo persica</i>
21	sbz39al	Asiatic lion	<i>Panthera leo persica</i>
22	humsk	Human	<i>Homo sapiens sapiens</i>
23	chimss	Chimpanzee	<i>Pan sp.</i>

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

sbz22al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	50
sbz38al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
sbz39al	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
adil.flesh	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCCTTCCAC	60
gz1nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCCTTCCAC	60
gz2nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCCTTCCAC	60
gz3nl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz23wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz28wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz22wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz20wt	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz63t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz56t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz26t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz30t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz45t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
bhz25t	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=14s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=15s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
d=16s1	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
gz21cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
gz22cl	TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCCTTCCAC	60
chimss	TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTTACCTTCCAC	60
humsk	TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTCCAC	60

sbz22al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz38al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
sbz39al	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCCTCCATGAA	120
adil.flesh	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz1nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz2nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
gz3nl	TTTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCCTCAGGAG	120
bhz23wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz28wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz22wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz20wt	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz63t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz56t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz26t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz30t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz45t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
bhz25t	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=14s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=15s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
d=16s1	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
gz21cl	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
gz22cl	TTTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCCTCCATGAG	120
chimss	TTTATCTTACCCTTTCATTATCAGCCCTAACCAACCTTCATCTCCTATTCTTACACGAA	120
humsk	TTTCATCTTGCCTTTCATTATTCAGCCCTAGCAGCAGTCCACCTCCTATTCTTGCACGAA	120
.. ..		
sbz22al	ACAGGATCTAA TAACCCCTCAGGAATGGTATCTGACTCAGATAAAA TTCCATTCCATCCA	190
sbz38al	ACAGGATCTAA TAACCCCTCAGGAATGGTATCTGACTCAGATAAAA TTCCATTCCATCCA	190


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bh228wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh222wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh220wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh263t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh256t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh226t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh230t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh245t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
bh225t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d214s1       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d215s1       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
d216s1       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCCTCTA 300
g221c1       GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCCGCCAACCCCTCTA 300
g222c1       GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCCGCCAACCCCTCTA 300
chimss       ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAATTATACCCTAGCTAACCCCTTA 300
humsk        ACACTATTCTCACCAGACCTCCTAGGCGACCCAGACAATTATACCCTAGCCAACCCCTTA 300

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sb222a1      AGCACCCCTCCCCATATCAAACCTGAAT 328
sb238a1      AGCACCCCTCCCCATATCAAACCTGAAT 328
sb239a1      AGCACCCCTCCCCATATCAAACCTGAAT 328
adil.flesh   AATACCCCTCCCCATATCAAGCCTGAAT 328
g21n1        AATACCCCTCCCCATATCAAGCCTGAAT 328
g22n1        AATACCCCTCCCCATATCAAGCCTGAAT 328
g23n1        AATACCCCTCCCCATATCAAGCCTGAAT 328
bh223wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh228wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh222wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh220wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bh263t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bh256t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bh226t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bh230t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bh245t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bh225t       AACACCCCTCCCCATATCAAGCGCGAAT 328
d214s1       AACACCCCTCCCCATATCAAGCCCGAAT 328
d215s1       AACACCCCTCCCCATATCAAGCCCGAAT 328
d216s1       AACACCCCTCCCCATATCAAGCCCGAAT 328
g221c1       AATACCCCTCCCCATATCAAGCCTGAAT 328
g222c1       AATACCCCTCCCCATATCAAGCCTGAAT 328
chimss       AACACCCCACCCCACATTAAACCCGAAT 328
humsk        AACACCCCTCCCCACATCAAGCCCGAAT 328

```

* * * * *

Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	C	G	C	T
gz1l
gz2l	C
gz3l	C
bhz25t	C	C	G	C
bhz26t	C	C	G	C
bhz30t	C	C	G	C
bhz45t	C	C	G	C
bhz56t	C	C	G	C
bhz20wt	C	C	G	C
bhz22wt	C	C	G	C
bhz23wt	C	C	G	C
dz14sl	C	C	C
dz15sl	C	C	C
sbz22al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
sbz38al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
gz21cl	T	C	T	.	C	T	.	C
gz22cl	T	C	T	.	C	T	.	C
chlmss	A	C	A	T	C	A	T	A	T	A	T	C	A	C	A	C	A	T	A	C
humsk	A	C	A	T	C	A	T	A	T	A	T	C	A	C	A	C	A	T	A	C

Table 8. Percent similarity matrix calculated by pair-wise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlmss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1			81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		86.9	79.6	81.1	80.2	80.2	79	81.4
chlmss	78.7	78.7	78.4	86.9		78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1		98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100		88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	88.1		89.6
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	

Table 10



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=

(25 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reportsDistribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

	Score	E
	(bits)	Value
gb AF231651.1 AF231651 Strongylura notata clone HB-82 cyto...	50	2e-05
gb AF231650.1 AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1 Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1 Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1 Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1 Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1 Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1 Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1 Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1 Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1 Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1 Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1 Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1 Poospiza boliviana cytochrome b (cytb) gene...	50	2e-05
gb AY005199.1 Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1 Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870 Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095 Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1 Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662 Gryllus campestris haplotype 2 cyto...	50	2e-05
gb AF248661.1 AF248661 Gryllus campestris haplotype 1 cyto...	50	2e-05
gb AF096462.1 AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb AF283644.1 AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283643.1 AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283642.1 AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283641.1 AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283640.1 AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb AF283639.1 AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
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gb AF283636.1 AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb AF283635.1 AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
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gb AF283633.1 AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb AF283632.1 AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb AF283631.1 AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
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gb AF283626.1 AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
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gb AF283622.1 AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb AF283621.1 AF283621 Elaphe obsoleta LSUMZ 37225 cytochro...	50	2e-05
gb AF283620.1 AF283620 Elaphe obsoleta LSUMZ 37163 cytochro...	50	2e-05
gb AF283619.1 AF283619 Elaphe obsoleta LSUMZ 37162 cytochrom...	50	2e-05
gb AF283618.1 AF283618 Elaphe obsoleta LSUMZ H15876 cytochr...	50	2e-05
gb AF283617.1 AF283617 Elaphe obsoleta LSUMZ H15872 cytochr...	50	2e-05
gb AF283616.1 AF283616 Elaphe obsoleta LSUMZ 15871 cytochro...	50	2e-05
gb AF283615.1 AF283615 Elaphe obsoleta LSUMZ H15870 cytochr...	50	2e-05
gb AF283614.1 AF283614 Elaphe obsoleta LSUMZ H15867 cytochr...	50	2e-05
gb AF283613.1 AF283613 Elaphe obsoleta LSUMZ H15864 cytochr...	50	2e-05

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck (<i>Antelope cervicapra</i>)	97, 58	96, 54
2	Sheep (<i>Ovis</i>	87, 53	96, 54
3	Pig (<i>Sus scrofa</i>)	87, 52	87, 41
4	Fresh water dolphin (<i>Platanista gangetica</i>)	86, 49	82, 47

Sequences producing significant alignments:

Score E
(bits) Value

gb AF231651.1 AF231651	Strongylura notata clone HB-82 cyto...	50	2e-05
gb AF231650.1 AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05
ref NC_002672.1	Dinornis giganteus mitochondrion, complete...	50	2e-05
ref NC_002673.1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AF232015.1 AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05
gb AF232013.1 AF232013	Bradypus variegatus cytochrome b gen...	50	2e-05
gb AY016015.1	Emeus crassus mitochondrion, complete genome	50	2e-05
gb AY016013.1	Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb AY016014.1	Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb AF230167.1 AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb AF074594.1 AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05
gb AY005210.1	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb AY005209.1	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb AY005208.1	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb AY005205.1	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb AY005204.1	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb AY005203.1	Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb AY005201.1	Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb AY005199.1	Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb AY005198.1	Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb AF155870.1 AF155870	Heterocephalus glaber cytochrome b (...)	50	2e-05
gb AF189123.1 AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb AF102099.1 AF102099	Criniferoides leucogaster cytochrome...	50	2e-05
gb AF102095.1 AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05
gb AF271065.1 AF271065	Mustela erminea specimen-voucher AF1...	50	2e-05
gb AF243857.1 AF243857	Strongylura notata notata cytochrome...	50	2e-05
gb AF243856.1 AF243856	Strongylura notata forsythia cytochr...	50	2e-05
ref NC_001567.1	Bos taurus mitochondrion, complete genome	50	2e-05
gb AF306872.1 AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306871.1 AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05
gb AF306870.1 AF306870	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306869.1 AF306869	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF306868.1 AF306868	Brachyramphus brevirostris haplotype...	50	2e-05
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	50	2e-05
gb AF248662.1 AF248662	Gryllus campestris haplotype 2 cyto...	50	2e-05
gb AF248661.1 AF248661	Gryllus campestris haplotype 1 cyto...	50	2e-05
gb AF096462.1 AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05
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gb AF283641.1 AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
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gb AF283578.1 AF283578	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
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gb AF290150.1 AF290150	Volatinia jacarina cytochrome b (cyt...	50	2e-05
gb AF176252.1 AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb AF176251.1 AF176251	Reithrodontomys zacatecae cytochrome...	50	2e-05
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gb AF163904.1 AF163904	Microtus pinetorum cytochrome b gene...	50	2e-05
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb AF163899.1 AF163899	Microtus miurus cytochrome b gene, c...	50	2e-05
gb AF163891.1 AF163891	Microtus californicus cytochrome B (...)	50	2e-05
gb AF163890.1 AF163890	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb AF288524.1 AF288524	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb AF288523.1 AF288523	Dipsochelys dussumieri isolate white...	50	2e-05
gb AF288522.1 AF288522	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb AF123530.1 AF123530	Psilopogon pyrolophus cytochrome b (...)	50	2e-05
gb AF123512.1 AF123512	Eubucco bourcierii cucinkae cytochro...	50	2e-05
gb AF206548.1 AF206548	Adolfus vauereselli cytochrome b gen...	50	2e-05
gb AF197857.1 AF197857	Gymnorhina tibicen cytochrome b gene...	50	2e-05
gb U63397.3 SEU63397	Sitta europaea cytochrome b gene, part...	50	2e-05
NC 001945.1	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
NC 001821.1	Dasypus novemcinctus mitochondrion, comple...	50	2e-05
gb AF141217.1 AF141217	Dasymys incommis country Tanzania cy...	50	2e-05
gb AF201615.1 AF201615	Pantodon buchholzi cytochrome b gene...	50	2e-05
gb AF077920.1 AF077920	Bombus nevadensis cytochrome b gene...	50	2e-05
gb AF190612.1 AF190612	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb J01124.1 BOVM780	taurus mitochondrion, complete genome	50	2e-05
gb AF191810.1 AF191810	Cochlearius cochlearius cytochrome b...	50	2e-05

gb U89181.1 CAU89181	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb U89171.1 AFU89171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb AF217833.1 AF217833	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb AF217822.1 AF217822	Hydrophis semperi cytochrome b gene,...	50	2e-05
gb AF217813.1 AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb AF220408.1 AF220408	Calliophis kelloggi cytochrome b (cy...	50	2e-05
gb AF126430.1 AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb AF090337.1 AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb AF059111.1 AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb AF059053.1 AF059053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb AF099308.1 AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb AF099295.1 AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb AF099294.1 AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb AF099293.1 AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb AF160610.1 AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb AF036280.1 AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb AF036277.1 AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb AF036274.1	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb AF194218.1 AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb AF194216.1 AF194216	Urosaurus ornatus cytochrome b gene,...	50	2e-05
ref NC 002009.1	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref NC 001941.1	Ovis aries mitochondrion, complete genome	50	2e-05
ref NC 000877.1	Aythya americana mitochondrion, complete g...	50	2e-05
ref NC 000845.1	Rhea americana mitochondrion, complete genome	50	2e-05
gb U27551.1 GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb AF089058.1 AF089058	Quiscalus quiscula cytochrome b (cyt...	50	2e-05
gb AF089055.1 AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb AF089054.1 AF089054	Quiscalus lugubris cytochrome b (cyt...	50	2e-05
gb AF089046.1 AF089046	Oreopsar bolivianus cytochrome b (cy...	50	2e-05
gb AF089042.1 AF089042	Molothrus badius cytochrome b (cytb)...	50	2e-05
gb AF089039.1 AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb AF089037.1 AF089037	Lamprosarpis tanagrinus cytochrome b (...)	50	2e-05
gb AF089026.1 AF089026	Gymnomystax mexicanus cytochrome b (...)	50	2e-05
gb AF089025.1 AF089025	Gnorimopsar chopi cytochrome b (cytb...	50	2e-05
gb AF089024.1 AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb AF089023.1 AF089023	Euphagus carolinus cytochrome b (cyt...	50	2e-05
gb AF089021.1 AF089021	Dives warstewiczii cytochrome b (cyt...	50	2e-05
gb AF089020.1 AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb AF089016.1 AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb AF089013.1 AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb AF089012.1 AF089012	Agelaius xanthomus cytochrome b (cyt...	50	2e-05
gb AF089008.1 AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb AF089006.1 AF089006	Agelaius humeralis cytochrome b (cyt...	50	2e-05
gb AF089005.1 AF089005	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb AF108695.1 AF108695	Scolomys jruaense cytochrome B (cyt...	50	2e-05
gb AF108685.1 AF108685	Wiedomys pyrrhorhinos cytochrome B (...)	50	2e-05
gb AF108677.1 AF108677	Thomasomys oreas cytochrome B (cytB)...	50	2e-05
gb AF145511.1 AF145511	Melanoplus foedus cytochrome b gene,...	50	2e-05
gb AF145511.1 AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb U89627.1 BMU89627	Bolitoglossa marmorata cytochrome b (cy...	50	2e-05
gb U89623.1 BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb AF181470.1 AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb AF084075.1 AF084075	Lagenorhynchus acutus cytochrome b g...	50	2e-05
gb U90303.1 OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90302.1 OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90301.1 OMU90301	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb U90300.1 OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb AF038883.1 AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb AF039269.1 AF039269	Agkistrodon concoloris cytochrome b ...	50	2e-05
gb AF039267.1 AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb S49215.1 S49215	apocytochrome b (sheep, domestic, Merino...	50	2e-05
gb AF158698.1 AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb AF158692.1 AF158692	Geomys butleri jugoslavicus cyto...	50	2e-05
gb AF058123.1 AF058123	Ichaginia cruentus cytochrome b (cyt...	50	2e-05
gb AF021629.1 AF021629	Antilocapra americana cytochrome b (...)	50	2e-05
gb AF022063.1	Tragelaphus strepsiceros cytochrome b (cytb)...	50	2e-05
gb AF022062.1	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb AF022060.1	Hippocragus equinus cytochrome b (cytb) gene...	50	2e-05
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	50	2e-05
gb AF111500.1 AF111500	Lagenorhynchus acutus isolate LAC074...	50	2e-05
gb AF111499.1 AF111499	Lagenorhynchus acutus isolate LAC073...	50	2e-05

gb U69744.1 LBUC69744	Lexocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb U69745.1 EMUC69745	Eunectes notaeus cytochrome b (cytb) g...	50	2e-05
gb U69746.1 EMUC69746	Eunectes murinus cytochrome b (cytb) g...	50	2e-05
gb U69747.1 ESU69747	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb U69748.1 ESU69748	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69749.1 ESU69749	Epicrates striatus strigilatus cytochr...	50	2e-05
gb U69750.1 ESU69750	Epicrates striatus mcrauniei cytochrom...	50	2e-05
gb U69751.1 ESU69751	Epicrates striatus mcrauniei cytochrom...	50	2e-05
gb U69752.1 EMUC69752	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69753.1 EMUC69753	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb U69754.1 EFUC69754	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb U69755.1 EFUC69755	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb U69756.1 ECUC69756	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69757.1 ECUC69757	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb U69758.1 EAU69758	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69759.1 EAU69759	Epicrates angulifer cytochrome b (cytb)...	50	2e-05
gb U69760.1 CEUC69760	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69761.1 CEUC69761	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69762.1 CEUC69762	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69763.1 CEUC69763	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb U69764.1 CAUC69764	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb U69765.1 BCUC69765	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb U69766.1 BCUC69766	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb AF139057.1 AF139057	Isodon macrourus cytochrome b gene,...	50	2e-05
gb AF090339.1 AF090339	Rhea americana mitochondrion, comple...	50	2e-05
gb AF006275.1 AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
gb AF006267.1 AF006267	Cnemidophorus tigris strain Isla Smi...	50	2e-05
gb AF034969.1 AF034969	Connochaetes taurinus cytochrome b g...	50	2e-05
gb AF028822.1 AF028822	Alcelaphus buselaphus cytochrome b g...	50	2e-05
gb AF028821.1 AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb AF061340.1 AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb AF076093.1 AF076093	Thalassarche impavida cytochrome b (...)	50	2e-05
gb AF076091.1 AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
gb AF076072.1 AF076072	Pelagodroma marina cytochrome b (cyt...	50	2e-05
gb AF076063.1 AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
gb AF076059.1 AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
gb AF076056.1 AF076056	Garrodia nareis cytochrome b (cytb) ...	50	2e-05
gb AF076053.1 AF076053	Fregatta tropica cytochrome b (cytb)...	50	2e-05
gb AF076050.1 AF076050	Diomedea gibsoni cytochrome b (cytb)...	50	2e-05
gb AF076049.1 AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb AF076048.1 AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
gb AF076047.1 AF076047	Diomedea antipodensis cytochrome b (...)	50	2e-05
gb U83314.1 MSU83314	Microstus semitorquatus cytochrome b (...)	50	2e-05
gb U83318.1 MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
gb U37303.1 SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb U37302.1 PAU37302	Ptychoramphus aleuticus cytochrome b g...	50	2e-05
gb U37296.1 CPU37296	Cyclorhynchus psittacula cytochrome b...	50	2e-05
gb U37289.1 BBU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U37286.1 APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb U37104.1 APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb U37087.1 ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb U87525.1 HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87524.1 HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87523.1 HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U87522.1 HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb U17864.1 STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb U17861.1 OAU17861	Oreamnos americanus cytochrome b gene...	50	2e-05
gb U17862.1 OMU17862	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb U65274.1 TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65267.1 TBU65267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65260.1 TBU65260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb U65101.1 PAU65101	Perognathus amplius cytochrome b (cytb)...	50	2e-05
gb AF034739.1 AF034739	Capra aegagrus cytochrome b (cytb) g...	50	2e-05
gb AF034738.1 AF034738	Capra caucasica cytochrome b (cytb) gen...	50	2e-05
gb AF034737.1 AF034737	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb AF034735.1 AF034735	Capra ibex cytochrome b (cytb) gene, mitoch...	50	2e-05
gb AF034730.1 AF034730	Ovis arles cytochrome b (cytb) gene...	50	2e-05
gb AF034727.1 AF034727	Ovis vignei cytochrome b (cytb) gene...	50	2e-05

gb AF034724.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene...	50	2e-05
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	50	2e-05
gb AF057132.1 AF057132	Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb U94805.1 TMU94805	Trogon melanurus cytochrome b gene, mi...	50	2e-05
gb U94804.1 TCU94804	Trogon comptus cytochrome b gene, mito...	50	2e-05
gb U94803.1 TVU94803	Trogon viridis cytochrome b gene, mito...	50	2e-05
gb AF006251.1 AF006251	Sericossypha albocristata cytochrome...	50	2e-05
gb AF006249.1 AF006249	Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb AF006238.1 AF006238	Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb AF006234.1 AF006234	Hemispingus acropileus cytochrome b...	50	2e-05
gb AF006226.1 AF006226	Cypsnagra hirundinacea cytochrome b...	50	2e-05
gb AF006215.1 AF006215	Chlorophanes spiza cytochrome b (cyt...	50	2e-05
gb AF006214.1 AF006214	Chlorochrysa calliparaea cytochrome...	50	2e-05
gb AF006213.1 AF006213	Calochaetes coccineus cytochrome b (...)	50	2e-05
gb AF006212.1 AF006212	Buthraupis montana cytochrome b (cyt...	50	2e-05
emb AJ293419.1 RRU293419	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293416.1 RPY293416	Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb AJ293415.1 RPY293415	Rupicapra pyrenaica parva mitochon...	50	2e-05
emb AJ293414.1 RPY293414	Rupicapra pyrenaica ornata mitochon...	50	2e-05
emb AJ293412.1 RRU293412	Rupicapra rupicapra rupicapra mito...	50	2e-05
emb AJ293418.1 CFA293418	Capra falconeri mitochondrial part...	50	2e-05
gb U07578.1 DCU07578	Dasyercus cristicauda mitochondrion c...	50	2e-05
emb AJ004180.1 HPAJ4180	Hydrobates pelagicus mitochondrial...	50	2e-05
emb Y15695.1 SMY15695	Schilbe mystus mitochondrial cytb gen...	50	2e-05
emb Y15697.1 EDY15697	Eutropius depressirostris mitochondri...	50	2e-05
emb Y15696.1 EDY15696	Eutropius depressirostris mitochondri...	50	2e-05
gb AF015035.1 AF015035	Steatocranus casuarinus 20 cytochrom...	50	2e-05
gb AF015761.1 AF015761	Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb AF015758.1 AF015758	Oreomystis mana cytochrome b (Cytb)...	50	2e-05
gb AF015756.1 AF015756	Vestiaria coccinea cytochrome b (Cyt...	50	2e-05
gb AF015754.1 AF015754	Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb U76052.1 DNU76052	Dromaius novaehollandiae cytochrome b...	50	2e-05
emb AJ236634.1 CGL236634	Clethrionomys glareolus mitochondr...	50	2e-05
gb U83158.1 POU83158	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83157.1 POU83157	Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb U83156.1 AAU83156	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83155.1 AAU83155	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83154.1 AAU83154	Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb U83156.1 CLU83156	Chelodina longicollis cytochrome b gen...	50	2e-05
emb AJ277676.1 ESC277676	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277675.1 ESC277675	Elaphe scalaris mitochondrial part...	50	2e-05
emb AJ277672.1 ELO277672	Elaphe longissima mitochondrial pa...	50	2e-05
emb AJ277671.1 ELO277671	Elaphe longissima mitochondrial pa...	50	2e-05
emb Y11832.1 MTNCOMGN	Dasyus novemcinctus complete mitoch...	50	2e-05
emb AJ388467.1 NBA388467	Nemacheilus barbatulus mitochondria...	50	2e-05
emb AJ388468.1 IME388468	Ictalurus melas mitochondrial cyt b...	50	2e-05
emb AJ388459.1 LDE388459	Leucaspius delineatus mitochondrial...	50	2e-05
gb U46167.1 SCU46167	Sciurus carolinensis cytochrome b gene...	50	2e-05
emb AJ245673.1 SIN245673	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245638.1 SIN245638	Schilbe intermedius partial mitoch...	50	2e-05
emb AJ245678.1 EDE245678	Eutropius depressirostris partial...	50	2e-05
emb AJ245677.1 EDE245677	Eutropius depressirostris partial...	50	2e-05
emb AJ245676.1 EDE245676	Eutropius depressirostris partial...	50	2e-05
emb AJ245675.1 EDE245675	Eutropius depressirostris partial...	50	2e-05
emb AJ245674.1 EDE245674	Eutropius depressirostris partial...	50	2e-05
emb Y16884.1 MTRACOMPL	Rhea americana complete mitochondria...	50	2e-05
gb U60768.1 PCU60768	Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb U48955.1 TMU48955	Thalassarche melanophris melanophris c...	50	2e-05
gb U48954.1 TCU48954	Thalassarche chrysostoma cytochrome b...	50	2e-05
gb U48944.1 TCU48944	Thalassarche chlorochymos chlorochym...	50	2e-05
gb U48943.1 PFU48943	Phoebastria palpebrata cytochrome b (cy...	50	2e-05
gb U48942.1 PFU48942	Phoebastria fusca cytochrome b (cytb) g...	50	2e-05
gb U48941.1 MGU48941	Macronectes giganteus cytochrome b (cy...	50	2e-05
gb U48947.1 DEU48947	Diomedea exulans dabbenena cytochrome...	50	2e-05
gb U48946.1 DEU48946	Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb U48949.1 DAU48949	Diomedea amsterdamensis cytochrome b (...)	50	2e-05
gb U55725.1 PRU55725	Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb U55509.1 APU55509	Artibeus planirostris cytochrome b (cy...	50	2e-05
gb U55507.1 AQU55507	Artibeus obscurus cytochrome b (cytb)...	50	2e-05
gb U55505.1 AQU55505	Artibeus obscurus cytochrome b (cytb)...	50	2e-05

gb U66505.1 ALUG6505	Artibeus lituratus cytochrome b (cytb)...	50	2e-05
gb U66504.1 AJU66504	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66503.1 AJU66503	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb U66502.1 AIU66502	Artibeus intermedius cytochrome b (cyt...	50	2e-05
gb U66501.1 AZU66501	Artibeus inopinatus cytochrome b (cytb...	50	2e-05
gb U66500.1 AHU66500	Artibeus hirsutus cytochrome b (cytb)...	50	2e-05
gb U66499.1 AFU66499	Artibeus fraterculus cytochrome b (cyt...	50	2e-05
gb U66498.1 AFU66498	Artibeus fimbriatus cytochrome b (cytb...	50	2e-05
gb U63061.1 BBU63061	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63060.1 BBU63060	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63059.1 BBU63059	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U63058.1 BBU63058	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb U58386.1 SJUS8386	Scolomys juruaense cytochrome b (cyt-b...	50	2e-05
gb L11905.1 CGYMTCTB9D	Cratogeomys gymnuris mitochondrial c...	50	2e-05
gb U34672.1 MNU34672	Metachirus nudicaudatus cytochrome b l...	50	2e-05
gb U34671.1 MNU34671	Metachirus nudicaudatus cytochrome b l...	50	2e-05
emb Y14951.1 MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb Y14371.1 MTCCCYTB	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb L11909.1 CGYMTCTB9H	Cratogeomys tylosinus mitochondrial...	50	2e-05
gb L11901.1 PPGMTCTB9B	Geomys bursarius juggosicularis mito...	50	2e-05
gb L11904.1 CGYMTCTB9C	Cratogeomys goldmani goldmani mitocho...	50	2e-05
emb X94928.1 SPCYTB	S. putorius mitochondrial DNA for cytoch...	50	2e-05
gb U46770.1 ARU46770	Anthus richardi cytochrome b gene, mit...	50	2e-05
gb U46769.1 ABU46769	Anthus berthelotii cytochrome b gene, ...	50	2e-05
gb U46183.1 SSU46183	Sciurus stramineus cytochrome b gene, ...	50	2e-05
emb Y10728.1 PSMY10728	P. schwarzi mitochondrial cytb gene, ...	50	2e-05
emb X95768.1 NLMCB	N. leucopterus mitochondrial cytochrome b...	50	2e-05
emb X95767.1 NGRIMCB	N. griseus mitochondrial cytochrome b gene	50	2e-05
emb X86763.1 MTVGCT26	V. gryphus mitochondrial cytb gene	50	2e-05
emb X86754.1 MTLCCYT17	L. crumeniferus mitochondrial cytb gene	50	2e-05
emb X86743.1 MTQACT6	C. aura mitochondrial cytb gene	50	2e-05
dbj AB035242.1 AB035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb X50946.1 MITDCB33	T. dorbignyi mitochondrial gene for c...	50	2e-05
emb AJ000029.1 MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb X82302.1 MIFFCYTB9	P. fasciata mitochondrial cytochrome ...	50	2e-05
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emb X56284.1 MIOACYTB	O. aries mitochondrion cytb gene for c...	50	2e-05
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emb X72005.1 MILWCYTB	L. weddelli mitochondrial gene for cyt...	50	2e-05
emb Y08814.1 MIHLCTB9	H. liberiensis mitochondrial cytochro...	50	2e-05
emb X50942.1 MIGTCB33	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb X56290.1 MIDDCYTB	D. dama mitochondrion cytb gene for cy...	50	2e-05
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emb AJ000024.1 MICCCYB24	Capreolus capreolus mitochondrial ...	50	2e-05
emb V00654.1 MIETXX	Bos taurus complete mitochondrial genome	50	2e-05
emb X36286.1 MIAACYTB3A	A. americana mitochondrion cytb gene ...	50	2e-05
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dbj AB030025.1 AB030025	Sciurus stramineus mitochondrial cy...	50	2e-05
gb U18258.1 SCU18258	Spharagemon campestris cytochrome b ge...	50	2e-05
gb U18257.1 SCU18257	Spharagemon coliare cytochrome b gene...	50	2e-05
gb U18253.1 TPU18253	Trimerotropis pistrinaria cytochrome b...	50	2e-05
gb U18250.1 CPU18250	Camnula pellucida cytochrome b gene, m...	50	2e-05
gb U17904.1 CCU17904	Circotectix carlinianus mitochondrion ...	50	2e-05
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dbj D82889.1 D82889	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
dbj D32195.1 CCRMTCB25	Capricornis sumatrensis mitochondrial...	50	2e-05
dbj D32191.1 CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
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dbj D84205.1 SHPMTCB8E	Sheep mitochondrial DNA for cytochrom...	50	2e-05
dbj D84201.1 SHPMTCB8C	Ovis musimon mitochondrial DNA for cy...	50	2e-05
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gb U08944.1 VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
gb U08941.1 PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb U08940.1 PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb X95775.1 ACMCB	A. cristatus mitochondrial cytochrome b gene	50	2e-05
emb X95774.1 ABMCB	A. bennettii mitochondrial cytochrome b gene	50	2e-05
emb X95764.1 AAMCB	A. albertisi mitochondrial cytochrome b gene	50	2e-05
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gb AF232021.1 AF232021	Tamandua tetradactyla clone 5 cytoch...	45	3e-04
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	45	3e-04
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<u>AF006212</u>	303	327
<u>AJ293419</u>	398	422
<u>AJ293416</u>	398	422
<u>AJ293415</u>	398	422
<u>AJ293414</u>	398	422
<u>AJ293412</u>	398	422
<u>AJ293418</u>	398	422
<u>U07578</u>	398	422
<u>AJ004180</u>	302	326
<u>Y15695</u>	432	456
<u>Y15697</u>	432	456
<u>Y15696</u>	432	456
<u>AF015035</u>	448	472
<u>AF015761</u>	303	327
<u>AF015758</u>	303	327
<u>AF015756</u>	303	327
<u>AF015754</u>	303	327
<u>U76052</u>	401	425
<u>AJ236814</u>	398	422
<u>U83158</u>	302	326
<u>U83157</u>	304	328
<u>U83156</u>	302	326
<u>U83155</u>	303	327
<u>U83154</u>	300	324
<u>U81356</u>	320	344
<u>AJ277676</u>	299	323
<u>AJ277675</u>	299	323
<u>AJ277672</u>	299	323
<u>AJ277671</u>	299	323
<u>Y11832</u>	14568	14592
<u>AJ388467</u>	305	329
<u>AJ388468</u>	305	329
<u>AJ388459</u>	305	329
<u>U46167</u>	398	422
<u>AJ245673</u>	400	424
<u>AJ245678</u>	400	424
<u>AJ245677</u>	400	424
<u>AJ245676</u>	400	424
<u>AJ245675</u>	400	424
<u>AJ245674</u>	400	424
<u>Y16884</u>	14038	14062
<u>U60768</u>	243	267
<u>U48955</u>	401	425
<u>U48954</u>	401	425
<u>U48944</u>	401	425
<u>U48943</u>	401	425
<u>U48942</u>	401	425
<u>U48941</u>	401	425

<u>U48947</u>	401	425
<u>U48946</u>	401	425
<u>U48948</u>	401	425
<u>U15725</u>	303	327
<u>U66508</u>	398	422
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<u>U66506</u>	398	422
<u>U66505</u>	398	422
<u>U66504</u>	398	422
<u>U66503</u>	398	422
<u>U66502</u>	398	422
<u>U66501</u>	398	422
<u>U66500</u>	398	422
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<u>U63060</u>	302	326
<u>U63059</u>	302	326
<u>U63058</u>	302	326
<u>U58386</u>	398	422
<u>L11905</u>	398	422
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<u>U34671</u>	398	422
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<u>L11901</u>	398	422
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<u>U46769</u>	302	326
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<u>X95767</u>	303	327
<u>X86763</u>	299	323
<u>X86754</u>	299	323
<u>X86743</u>	299	323
<u>AB035242</u>	398	422
<u>X60946</u>	302	326
<u>AJ000029</u>	398	422
<u>X82302</u>	398	422
<u>X56291</u>	398	422
<u>X56284</u>	398	422
<u>AJ000022</u>	398	422
<u>X72005</u>	398	422
<u>Y08814</u>	398	422
<u>X60942</u>	302	326
<u>X56290</u>	398	422
<u>AJ000021</u>	398	422
<u>AJ000024</u>	398	422
<u>V00654</u>	14911	14915
<u>X56286</u>	398	422
<u>L19718</u>	398	422
<u>U27543</u>	401	425
<u>AB030025</u>	343	367
<u>U18258</u>	169	193
<u>U18257</u>	169	193
<u>U18253</u>	169	193
<u>U18250</u>	169	193
<u>U17904</u>	169	193
<u>DB4202</u>	398	422
<u>DB2889</u>	398	422
<u>Q12195</u>	243	267
<u>Q12191</u>	398	422
<u>AB021098</u>	198	422
<u>AB021097</u>	198	422
<u>AB021095</u>	198	422
<u>AB021094</u>	198	422
<u>AB021092</u>	198	422
<u>AB021091</u>	198	422

<u>AB001612</u>	398	422
<u>D84205</u>	398	422
<u>D84203</u>	398	422
<u>D14636</u>	398	422
<u>D14635</u>	398	422
<u>D12198</u>	243	267
<u>D12196</u>	243	267
<u>D12192</u>	398	422
<u>AB021099</u>	398	422
<u>AB021096</u>	398	422
<u>AB021093</u>	398	422
<u>AB021090</u>	398	422
<u>AB008539</u>	15302	15326
<u>AB006800</u>	398	422
<u>L12763</u>	260	284
<u>L08032</u>	401	425
<u>L28941</u>	398	422
<u>L28937</u>	398	422
<u>AJ010056</u>	269	293
<u>AJ010054</u>	269	293
<u>AJ010053</u>	269	293
<u>AJ010052</u>	269	293
<u>AJ010051</u>	269	293
<u>AJ010050</u>	269	293
<u>AJ010049</u>	269	293
<u>AJ010048</u>	269	293
<u>AJ010047</u>	269	293
<u>X95777</u>	407	431
<u>AJ009879</u>	269	293
<u>AJ010055</u>	269	293
<u>U08946</u>	303	327
<u>U08945</u>	303	327
<u>U08944</u>	303	327
<u>U08941</u>	303	327
<u>U08940</u>	303	327
<u>X95775</u>	303	327
<u>X95774</u>	303	327
<u>X95764</u>	303	327
<u>AF040383</u>	287	310
<u>AF232023</u>	400	422
<u>AF232022</u>	400	422
<u>AF232021</u>	400	422
<u>AF157466</u>	322	344
<u>AF157465</u>	324	346
<u>AF157464</u>	324	346
<u>AF157463</u>	324	346
<u>AF157460</u>	321	343
<u>AF231664</u>	400	422
<u>AF231663</u>	400	422
<u>AF231662</u>	400	422
<u>AF231660</u>	400	422
<u>AF231659</u>	400	422
<u>AF231658</u>	400	422
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<u>AF231644</u>	400	422
<u>AF231639</u>	400	422
<u>AF232019</u>	400	422
<u>AF232017</u>	400	422
<u>AF232014</u>	400	422
<u>AF118564</u>	345	367
<u>AF118563</u>	345	367
<u>AF118562</u>	344	366
<u>AF118561</u>	344	366
<u>AF118560</u>	344	366
<u>AF118559</u>	344	366
<u>AF118558</u>	344	366
<u>AF118557</u>	381	403
<u>AF118556</u>	381	403
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<u>AF118551</u>	381	403
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<u>AF118549</u>	381	403
<u>AF118548</u>	381	403
<u>AF238041</u>	400	422
<u>AF326272</u>	400	422
<u>AF326271</u>	400	422
<u>AF326270</u>	400	422
<u>AF326266</u>	400	422
<u>AJ004340</u>	302n.....	326
<u>AJ004264</u>	302n.....	326

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 39355
 Number of Sequences: 807597
 Number of extensions: 39355
 Number of successful extensions: 15066
 Number of sequences better than 10.0: 5706
 length of query: 25
 length of database: 2,863,827,885
 effective HSP length: 17
 effective length of query: 8
 effective length of database: 2,850,098,736
 effective search space: 22800789888
 effective search space used: 22800789888
 T: 0
 A: 30
 X1: 6 (11.9 bits)
 X2: 15 (29.7 bits)
 S1: 12 (24.3 bits)
 S2: 16 (32.2 bits)

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.



BLASTN 2.1.2 [Nov-13-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query-

(26 letters)

Database: nt

807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

qb AF189111.1 AF189111	Cryptotermes austrinus cytochrome b ...	52	6e-06
qb U86834.1 U86834	Phyllosticta wolffsohni MSB 67270 cytochrom...	52	6e-06
qb AF123633.1 AF123633	Perissoccephalus tricolor cytochrome ...	52	6e-06
qb AF123617.1 AF123617	Pipreola arcuata cytochrome b gene, ...	52	6e-06
qb AF127202.1 AF127202	Hylopetes fulviventris cytochrome b ...	52	6e-06
qb AF127194.1 AF127194	Grallaria guatemalensis cytochrome b...	52	6e-06
qb AF217828.1 AF217828	Aspidelaps scutatus cytochrome b gen...	52	6e-06
qb AF160578.1 AF160578	Hypogeomys antimenae Hant555 cytochro...	52	6e-06
qb AF009931.2 AF009931	Archocentrus centrarchus cytochrome ...	52	6e-06
qb AF091629.1 AF091629	Antilocapra americana cytochrome b (...	52	6e-06
qb AF034967.1	Sigmoceros lichtensteinii cytochrome b gene,...	52	6e-06
qb AF038290.1 AF038290	Antechinus sp. cytochrome b gene, mi...	52	6e-06
qb U07577.1 AMU07577	Antechinus melanurus mitochondrion cyt...	52	6e-06
qb U81343.1 CFU81343	Chelus fimbriata cytochrome b gene, mi...	52	6e-06
emb AJ222681.1 ABCYT08	Alcelaphus buselaphus mitochondrial ...	52	6e-06
qb M99464.1 PNZMTCYT8	Planigale sp. cytochrome b gene, comp...	52	6e-06
emb AJ225116.1 DNJ225116	Dryomys nitedula mitochondrial gen...	52	6e-06
qb U25738.1 PRU25738	Paradisaea raggiana cytochrome b gene,...	52	6e-06
qb U25736.1 PRU25736	Paradisaea rubra cytochrome b gene, mi...	52	6e-06
qb U15202.1 SMU15202	Seleucidis melanoleuca mitochondrion c...	52	6e-06
qb U15204.1 PR15204	Paradisaea raggiana mitochondrion cytoc...	52	6e-06
emb X56290.1 MIDDCYT8	D.dama mitochondrion cytb gene for cy...	52	6e-06
emb X56286.1 MIAACYT8A	A.americana mitochondrion cytb gene ...	52	6e-06
dbj D88639.1 D88639	Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj D82890.1 D82890	Bubalus depressicornis mitochondrial DN...	52	6e-06
qb AF119261.1 AF119261	Peromyscus maniculatus cytochrome b ...	46	3e-04
qb AF123615.1 AF123615	Rupicola rupicola cytochrome b gene,...	46	3e-04
qb AF160603.1 AF160603	Apodemus sylvaticus Asyl588 cytochro...	46	3e-04
qb U62697.1 CCOLCYT82	Charadrius collaris cytochrome b (cyt...	46	3e-04
qb U62685.1 CSICCYT82	Charadrius bicinctus cytochrome b (Cy...	46	3e-04
qb AF022071.1	Madoqua guentheri cytochrome b (cytb) gene, ...	46	3e-04
qb AF022070.1	Madoqua kirkii cytochrome b (cytb) gene, mit...	46	3e-04
qb U83317.1 PSU83317	Polihierax semitorquatus cytochrome b ...	46	3e-04
qb U37293.1 CCU37293	Cephus columba cytochrome b gene, mit...	46	3e-04
qb U37292.1 CCU37292	Cephus carbo cytochrome b gene, mitoc...	46	3e-04
qb U37291.1 SMU37291	Brachyramphus marmoratus perdix cytoch...	46	3e-04
qb AF082055.1 AF082055	Rupicola rupicola cytochrome b gene,...	46	3e-04
qb U72770.1 JMU72770	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
qb U07578.1 DCU07578	Dasyercus cristicauda mitochondrion c...	46	3e-04
qb AF031908.1 GOCCTCYT83	Geopsittacus occidentalis cytochrom...	46	3e-04
emb AJ004231.1 SBAJ4231	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004230.1 SBAJ4230	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004229.1 SBAJ4229	Sula bassana mitochondrial cytb gen...	46	3e-04
emb AJ004232.1 SBAJ4232	Sula bassana mitochondrial cytb gen...	46	3e-04
qb U88865.1	Pomacentrus sp. cytochrome b (cytb) gene, mito...	46	3e-04
qb U90001.1 MSU90001	Morus bassanus cytochrome b gene, mito...	46	3e-04
qb U63057.1 SMU63057	Brachyramphus marmoratus perdix cytoch...	46	3e-04
dbj AB036404.1 AB036404	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036402.1 AB036402	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036400.1 AB036400	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj AB036398.1 AB036398	Rana porosa porosa mitochondrial DN...	46	3e-04
qb U19611.1 JMU19611	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
emb X22519.1 HACTY8	H.ampullatus cytochrome b gene (comple...	46	3e-04
qb U08014.1 GAEMTCYT8A	Galeocerdo cuvier mitochondrial cyto...	46	3e-04
qb U08013.1 CPLMTCYT88	Carcharias porosus mitochondrial c...	46	3e-04
qb AY015012.1	Crypturellus tataupa mitochondrion, partial ...	44	0.001
qb AF074591.1 AF074591	Petrochelidon pyrrhonota cytochrome ...	44	0.001
qb AY005212.1	Pooeciza whitii isolate 2 cytochrome b (cytb)...	44	0.001
qb AY005211.1	Pooeciza whitii isolate 1 cytochrome b (cytb)...	44	0.001
qb AF187132.1 AF187132	Cryptotermes tropicalis cytochrome b...	44	0.001
qb AF187130.1 AF187130	Cryptotermes secundus cytochrome b (...	44	0.001
qb AF187119.1 AF187119	Cryptotermes primus isolate 2 cytoch...	44	0.001
qb AF187117.1 AF187117	Cryptotermes primus isolate 1 cytoch...	44	0.001
qb AF187115.1 AF187115	Cryptotermes dudleyi cytochrome b (Cy...	44	0.001
qb AF112197.1 AF112197	Ovis canadensis cytochrome b gene, p...	44	0.001
qb AF112197.1 AF112197	Ovis canadensis canadensis cytochrom...	44	0.001
qb AF112199.1 AF112199	Ovis canadensis nelsoni cytochrome b ...	44	0.001
qb AF291272.1 AF291272	Vireo cacaecia cacaecia apoclinus...	44	0.001

gb AF081989.1 AF081989	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081988.1 AF081988	Vireo cassinii cassinii specimen-vou...	44	0.001
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gb AF081982.1 AF081982	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081981.1 AF081981	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081980.1 AF081980	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081979.1 AF081979	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081978.1 AF081978	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081977.1 AF081977	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081976.1 AF081976	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081975.1 AF081975	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081974.1 AF081974	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081973.1 AF081973	Vireo cassinii cassinii specimen-vou...	44	0.001
gb AF081972.1 AF081972	Vireo cassinii cassinii specimen-vou...	44	0.001
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gb AF081970.1 AF081970	Vireo solitarius alticola country US...	44	0.001
gb AF081969.1 AF081969	Vireo solitarius alticola country US...	44	0.001
gb AF081968.1 AF081968	Vireo solitarius alticola country US...	44	0.001
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gb AF081966.1 AF081966	Vireo solitarius solitarius specimen...	44	0.001
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gb AF081964.1 AF081964	Vireo solitarius solitarius specimen...	44	0.001
gb AF081962.1 AF081962	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081961.1 AF081961	Vireo flavifrons specimen-voucher LS...	44	0.001
gb AF081960.1 AF081960	Vireo leucophrys leucophrys specimen...	44	0.001
gb AF081959.1 AF081959	Vireolanius leucotis leucotis cytoch...	44	0.001
gb AF112405.2 AF112405	Barbus anoplus cytochrome b (cytb) g...	44	0.001
gb AF144317.1 AF144317	Amphiprion ocellaris isolate 3 haplo...	44	0.001
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gb AF144313.1 AF144313	Amphiprion ocellaris isolate 1 haplo...	44	0.001
gb AF144312.1 AF144312	Amphiprion ocellaris haplotype 3DH12...	44	0.001
gb AF144311.1 AF144311	Amphiprion ocellaris haplotype 3DH1...	44	0.001
gb AF144310.1 AF144310	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb AF144309.1 AF144309	Amphiprion ocellaris isolate 1 haplo...	44	0.001
ref NC 001567.1	Bos taurus mitochondrion, complete genome	44	0.001
gb AF212124.1 AF212124	Anolis schwartzi cytochrome b gene, ...	44	0.001
gb AF182706.1 AF182706	Phapitreron amethystina cytochrome b...	44	0.001
gb AF010406.1 AF010406	Ovis aries complete mitochondrial ge...	44	0.001
gb AF096452.1 AF096452	Platysteira cyanea cytochrome b gene...	44	0.001
gb AF281619.1 AF281619	Elaphe obsoleta LSUMZ39162 cytochrom...	44	0.001
gb AF281618.1 AF281618	Elaphe obsoleta LSUMZ H15896 cytochr...	44	0.001
gb AF281608.1 AF281608	Elaphe obsoleta LSUMZ H14782 cytochr...	44	0.001
gb AF281602.1 AF281602	Elaphe obsoleta LSUMZ H3388 cytochro...	44	0.001
gb AF310069.1 AF310069	Elaenia martinica cytochrome b gene...	44	0.001
gb AF146616.1 AF146616	Actophilornis africanus cytochrome b...	44	0.001
gb AF271410.1 AF271410	Galago moholi cytochrome b (cyt b) g...	44	0.001
gb AF290139.1 AF290139	Peucedramus taeniatus cytochrome b (...)	44	0.001
ref NC 002504.1	Lama pacos mitochondrion, complete genome	44	0.001
gb AF163901.1 AF163901	Microtus ochrogaster cytochrome b ge...	44	0.001
gb AF119253.1 AF119253	Myopus schisticolor cytochrome b gen...	44	0.001
gb AF119259.1 AF119259	Synaptomys borealis cytochrome b gen...	44	0.001
gb AF288454.1 AF288454	Nyctereutes procyonoides korensis c...	44	0.001
gb AF163895.1 AF163895	Microtus gregalis cytochrome B (cytB...	44	0.001
gb AF123647.1 AF123647	Machaeropterus regulus scutellatus cy...	44	0.001
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gb AF123637.1 AF123637	Rupicola peruviana cytochrome b gene...	44	0.001
gb AF123636.1 AF123636	Oellonnia scleracti cytochrome b gene...	44	0.001

<u>gb AF127201.1 AF127201</u>	<u>Myrmothera campanisona cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF127192.1 AF127192</u>	<u>Grallaria ruficapilla cytochrome b g...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF127189.1 AF127189</u>	<u>Grallaria varia cytochrome b gene, p...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF197849.1 AF197849</u>	<u>Sericornis frontalis cytochrome b ge...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF197847.1 AF197847</u>	<u>Pardalotus striatus cytochrome b gen...</u>	<u>44</u>	<u>0.001</u>
<u>ref NC 000889.1 </u>	<u>Hippopotamus amphibius mitochondrion, comp...</u>	<u>44</u>	<u>0.001</u>
<u>ref NC 002079.1 </u>	<u>Carassius auratus mitochondrion, complete ...</u>	<u>44</u>	<u>0.001</u>
<u>ref NC 001794.1 </u>	<u>Macropus robustus mitochondrion, complete ...</u>	<u>44</u>	<u>0.001</u>
<u>ref NC 001610.1 </u>	<u>Didelphis virginiana mitochondrion, comple...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF201612.1 AF201612</u>	<u>Stomatorhinus sp. CU79703 cytochrome...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF097931.1 AF097931</u>	<u>Amphiprion clarkii cytochrome b gene...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF097927.1 AF097927</u>	<u>Amphiprion ocellaris cytochrome b ge...</u>	<u>44</u>	<u>0.001</u>
<u>gb J01394.1 BOVMT</u>	<u>Bos taurus mitochondrion, complete genome</u>	<u>44</u>	<u>0.001</u>
<u>gb AF168760.1 AF168760</u>	<u>Apalone spinifera isolate TXsc cytoc...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF168759.1 AF168759</u>	<u>Apalone spinifera isolate TXki cytoc...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF168758.1 AF168758</u>	<u>Apalone spinifera isolate TXcc cytoc...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF168756.1 AF168756</u>	<u>Apalone spinifera isolate NMrg cytoc...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF182381.1 AF182381</u>	<u>Petrochelidon rufocollaris isolate E...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF182380.1 AF182380</u>	<u>Petrochelidon rufocollaris isolate E...</u>	<u>44</u>	<u>0.001</u>
<u>gb U89187.1 MMU89187</u>	<u>Momotus mexicanus cytochrome b (cytb) ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF193833.1 AF193833</u>	<u>Botaurus lentiginosus cytochrome b g...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF193822.1 AF193822</u>	<u>Ardea alba cytochrome b gene, partia...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF193821.1 AF193821</u>	<u>Ardea herodias cytochrome b gene, pa...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217837.1 AF217837</u>	<u>Paranaja multifasciata cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217835.1 AF217835</u>	<u>Naja kaouthia cytochrome b gene, com...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217834.1 AF217834</u>	<u>Laticauda colubrina cytochrome b gen...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217831.1 AF217831</u>	<u>Calliophis japonicus cytochrome b ge...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217823.1 AF217823</u>	<u>Micruroides euryxanthus cytochrome b...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217819.1 AF217819</u>	<u>Drysdalia coronata cytochrome b gene...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF217815.1 AF217815</u>	<u>Austrelaps superbus cytochrome b gen...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF118156.1 AF118156</u>	<u>Teranura humeralis specimen-voucher ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF209938.1 AF209938</u>	<u>Euura atra isolate 62 cytochrome b g...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF209933.1 AF209933</u>	<u>Euura atra isolate C cytochrome b ge...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF059104.1 AF059104</u>	<u>Marmaronetta angustirostris cytochro...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF059102.1 AF059102</u>	<u>Lophonetta specularoides cytochrome ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF059054.1 AF059054</u>	<u>Amazonetta brasiliensis cytochrome b...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF192646.1 AF192646</u>	<u>Hippocampus barbouri haplotype PH.22...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF192645.1 AF192645</u>	<u>Hippocampus barbouri haplotype PH.13...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160614.1 AF160614</u>	<u>Cricetomys gambianus Cgam518 cytochr...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160613.1 AF160613</u>	<u>Cricetomys emini Cemi511 cytochrome ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160612.1 AF160612</u>	<u>Cricetomys emini Cemi530 cytochrome ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160611.1 AF160611</u>	<u>Cricetomys emini Cemi637 cytochrome ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160610.1 AF160610</u>	<u>Cricetomys emini Cemi636 cytochrome ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160604.1 AF160604</u>	<u>Calomyscus bailwardi Cbal576 cytochr...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160560.1 AF160560</u>	<u>Eliurus majori Emaj642 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160559.1 AF160559</u>	<u>Eliurus majori Emaj641 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160558.1 AF160558</u>	<u>Eliurus majori Emaj639 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160557.1 AF160557</u>	<u>Eliurus majori Emaj638 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160555.1 AF160555</u>	<u>Eliurus majori Emaj614 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160554.1 AF160554</u>	<u>Eliurus majori Emaj617 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160553.1 AF160553</u>	<u>Eliurus majori Emaj573 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160552.1 AF160552</u>	<u>Eliurus majori Emaj556 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160551.1 AF160551</u>	<u>Eliurus majori Emaj561 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160550.1 AF160550</u>	<u>Eliurus majori Emaj443 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF160549.1 AF160549</u>	<u>Eliurus majori Emaj444 cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016287.1 AF016287</u>	<u>Damaliscus pygargus cytochrome b (cy...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016286.1 AF016286</u>	<u>Oryx leucoryx cytochrome b (cytb) ge...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016283.1 AF016283</u>	<u>Antelope cervicapra cytochrome b (cy...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016281.1 AF016281</u>	<u>Antidorcas marsupialis cytochrome b ...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016278.1 AF016278</u>	<u>Tragelaphus oryx cytochrome b (cytb)...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016275.1 AF016275</u>	<u>Tragelaphus eucyceros cytochrome b (...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF016274.1 </u>	<u>Tetracerus quadricornis cytochrome b (cytb) ...</u>	<u>44</u>	<u>0.001</u>
<u>ref NC 001941.1 </u>	<u>Ovis aries mitochondrion, complete genome</u>	<u>44</u>	<u>0.001</u>
<u>gb AF109699.1 AF109699</u>	<u>Microcyzomys minutus cytochrome b (c...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF109692.1 AF109692</u>	<u>Rhipidomys nitela cytochrome b (cytb...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF109677.1 AF109677</u>	<u>Thomomys daphne cytochrome b (cytb...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF109652.1 AF109652</u>	<u>Scapteromys tumidus cytochrome b (cy...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF042722.1 AF042722</u>	<u>Megamuntiacus vuquangensis cytochrom...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF042719.1 </u>	<u>Muntiacus muntjak cytochrome b gene, mitoch...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF042718.1 AF042718</u>	<u>Stenella coeruleoalba cytochrome b g...</u>	<u>44</u>	<u>0.001</u>
<u>gb AF042717.1 AF042717</u>	<u>Stenella coeruleoalba cytochrome b g...</u>	<u>44</u>	<u>0.001</u>

gb AF084074.1 AF084074	Lagenorhynchus albirostris cytochrom...	44	0.001
gb AF090750.1 AF090750	Gobio gobio balcanicus cytochrome b ...	44	0.001
gb AF157939.1 AF157939	Spermophilus columbianus columbianus...	44	0.001
gb AF157937.1 AF157937	Spermophilus washingtoni isolate S89...	44	0.001
gb AF157936.1 AF157936	Spermophilus washingtoni isolate S88...	44	0.001
gb AF157915.1 AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb AF157914.1 AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb AF157912.1 AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb AF157906.1 AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb AF157891.1 AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb AF157882.1 AF157882	Spermophilus columbianus columbianus...	44	0.001
gb AF157859.1 AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb AF157858.1 AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb AF157839.1 AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb AF030497.1 AF030497	Crocridura brunnea cytochrome b (cyt ...	44	0.001
gb U03541.2 LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb AF009951.2 AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb AF009941.1 AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb AF009925.1 AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
gb AF094633.1 AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb AF094621.1 AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb AF094618.1 AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb AF166348.1 AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb AF158697.1 AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb AF158694.1 AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb AF158693.1 AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb AF158688.1 AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb AF100720.1 AF100720	Spermophilus citellus cytochrome b (...	44	0.001
gb AF091632.1 AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb AF102815.1 AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb AF102814.1 AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb AF022065.1	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb AF022059.1	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb AF022058.1	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb AF022057.1	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb AF022054.1	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb AF016637.1 AF016637	Connochaetes gnou cytochrome b (cytb...	44	0.001
gb U69863.1 PSU69863	Python sebae cytochrome b (cytb) gene,...	44	0.001
gb U69844.1 LTU69844	Lichanura trivirgata cytochrome b (cyt...	44	0.001
gb AF143193.1 AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb AF121222.1 AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb AF096625.1 AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb AF096624.1 AF096624	Kobus ellipsiprymnus ellipsiprymnus c...	44	0.001
gb AF081052.1 AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb AF081049.1 AF081049	Eulemur macaco macaco cytochrome b (...	44	0.001
gb AF081048.1 AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb AF082063.1 AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb AJ010957.1 HAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb U76506.1 CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb U76504.1 CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb U76505.1 ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb U76503.1 APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb U76508.1 AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb AF034969.1 AF034969	Connochaetes taurinus cytochrome b g...	44	0.001
gb AF051876.1 AF051876	Rhodeus ocellatus cytochrome b (cytb...	44	0.001
gb AF082007.1 AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb AF082006.1 AF082006	Vireo plumbeus plumbeus specimen-vou...	44	0.001
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gb AF082004.1 AF082004	Vireo plumbeus plumbeus specimen-vou...	44	0.001
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gb AF081980.1 AF081980	Vireo plumbeus plumbeus specimen-vou...	44	0.001

gb AF081991.1 AF081991	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb S73150.1 S73150	cytochrome b (Spermophilus richardsonii-...	44	0.001
gb AF012235.1 AF012235	Cryptomys hottentotus natalensis cyt...	44	0.001
gb U53580.1 NCU53580	Nycticebus coucang cytochrome b (cyt b...	44	0.001
gb U53577.1 EFU53577	Eulemur fulvus rufus cytochrome b (cyt...	44	0.001
gb U53576.1 EFU53576	Eulemur fulvus collaris cytochrome b (...	44	0.001
gb U95512.1 ESERCYTB2	Eptesicus serotinus 3' cytochrome b (...	44	0.001
gb U95508.1 PKUHLCTB2	Pipistrellus kuhli 5' cytochrome b (...	44	0.001
gb U17868.1 BTU17868	Budorcas taxicolor taxicolor cytochrom...	44	0.001
gb U17867.1 BTU17867	Budorcas taxicolor bedfordi cytochrome...	44	0.001
gb U17860.1 ODU17860	Ovis dalli cytochrome b gene, mitochon...	44	0.001
gb U17859.1 OCU17859	Ovis canadensis cytochrome b gene, mit...	44	0.001
emb AJ010556.1 ASP010556	Acomys spinosissimus mitochondrial...	44	0.001
gb AF034736.1 AF034736	Capra falconeri cytochrome b (cytb) ...	44	0.001
gb AF034730.1 AF034730	Ovis aries cytochrome b (cytb) gene,...	44	0.001
gb AF034729.1 AF034729	Ovis vignei cytochrome b (cytb) gene...	44	0.001
gb AF034728.1	Ovis dalli dalli cytochrome b (cytb) gene, m...	44	0.001
gb AF034727.1	Ovis ammon darwini cytochrome b (cytb) gene,...	44	0.001
gb AF034724.1 AF034724	Pantholops hodgsoni cytochrome b (cy...	44	0.001
gb AF034722.1 AF034722	Addax nasomaculatus cytochrome b (cy...	44	0.001
gb U72038.1 MMU72038	Monodon monoceros cytochrome b (cytb)...	44	0.001
gb U72037.1 DLU72037	Delphinapterus leucas cytochrome b (Cy...	44	0.001
gb M99455.1 MURMTCYTB	Murexia longicaudata cytochrome b gen...	44	0.001
gb L29055.1 SHPMTDLOOP	Sheep mitochondrial cytochrome b (Cy...	44	0.001
gb AF082047.1 AF082047	Coccyzus americanus cytochrome b gen...	44	0.001
gb AF038286.1 AF038286	Antechinus minimus cytochrome b gene...	44	0.001
gb AF038284.1 AF038284	Antechinus swainsonii cytochrome b g...	44	0.001
gb AF059093.1 AF059093	Anas undulata cytochrome b gene, par...	44	0.001
gb AF059092.1 AF059092	Anas superciliosa rogersi cytochrome...	44	0.001
gb AF059091.1 AF059091	Anas sparsa cytochrome b gene, parti...	44	0.001
gb AF059080.1 AF059080	Anas melleri cytochrome b gene, part...	44	0.001
gb AF059078.1 AF059078	Anas laysanensis cytochrome b gene, ...	44	0.001
gb AF052240.1 AF052240	Anaïretes flavirostris cytochrome b ...	44	0.001
gb AF006240.1 AF006240	Mitrospingus cassinii cytochrome b (...	44	0.001
gb AF006227.1 AF006227	Dacnis cayana cytochrome b (cytb) ge...	44	0.001
gb AF047447.1 AF047447	Oryx leucoryx cytochrome b gene, mit...	44	0.001
gb U07576.1 AHU07576	Antechinus habbema mitochondrion cytoc...	44	0.001
gb AF028180.1 AF028180	Urocyon cinereoargenteus cytochrome ...	44	0.001
gb AF028178.1 AF028178	Pseudalopex sechurae cytochrome b (c...	44	0.001
gb AF028170.1 AF028170	Vulpes zerda cytochrome b (cytb) gen...	44	0.001
gb M99454.1 ASWMTSCYTB	Antechinus stuartii cytochrome b gen...	44	0.001
gb M99453.1 ASWMTCYTB	Antechinus swainsonii cytochrome b ge...	44	0.001
gb U23461.1 ANU23461	Antechinus naso cytochrome b gene, mit...	44	0.001
gb U87138.1 TVU87138	Trichosurus vulpecula cytochrome b (cy...	44	0.001
gb U07590.1 PMU07590	Planigale maculata mitochondrion cytoc...	44	0.001
emb AJ004326.1 PTAJ4326	Phylloscopus trochilus mitochondria...	44	0.001
gb AF020255.1 AF020255	Cyclura nubila cytochrome b (cytb) g...	44	0.001
emb Y19184.1 LPA19184	Lama pacos complete mitochondrial genome	44	0.001
gb U88862.1	Amphilophus citrinellum cytochrome b (cytb) ge...	44	0.001
gb U88859.1	Thorichthys aureum cytochrome b (cytb) gene, m...	44	0.001
gb U88858.1	Thorichthys cf. aureum cytochrome b (cytb) gen...	44	0.001
gb U88857.1	Herichthys labridens cytochrome b (cytb) gene...	44	0.001
gb U88856.1	Herichthys carpintis cytochrome b (cytb) gene...	44	0.001
emb Y10524.1 MIMROGEN	Macropus robustus complete mitochondri...	44	0.001
gb U81357.1 CSU81357	Chelydra serpentina cytochrome b gene...	44	0.001
gb U81356.1 CLU81356	Chelodina longicollis cytochrome b gen...	44	0.001
gb U75354.1 LUU75354	Leptomys mexicanus cytochrome b gene...	44	0.001
gb U77332.1 GCU77332	Gymnorhinus cyanocephalus cytochrome-b ...	44	0.001
emb Z29573.1 QVMTGNME	Didelphis virginiana complete mitoch...	44	0.001
emb AJ222679.1 BTCYTQ8	Boselaphus tragocamelus mitochondria...	44	0.001
emb AJ222680.1 TSCYTQ8	Tragelaphus spekei mitochondrial cyt...	44	0.001
emb AJ222685.1 ODCCTQ8	Oryx dammah mitochondrial cytochrome...	44	0.001
gb M22466.1 PMLMTCYTB	Perameles nasuta cytochrome b gene, c...	44	0.001
gb M22453.1 TQVMTCTB	Thylacinus cynocephalus cytochrome b ...	44	0.001
gb M22450.1 QAVMTCTB	Dasyurus hallucatus cytochrome b gene...	44	0.001
gb U25737.1 PMU25737	Paradisea minor cytochrome b gene, m...	44	0.001
gb U15203.1 PRU15203	Paradisea rudolphi mitochondrion cyto...	44	0.001
gb U15205.1 EAU15205	Epimachus albertii mitochondrion cyto...	44	0.001
gb U15209.1 PRU15209	Diphyllodes republica mitochondrion c...	44	0.001
emb AJ000424.1 STA424	Sorex tundrensis partial mitochondri...	44	0.001
emb AJ000423.1 STA423	Sorex tundrensis partial mitochondri...	44	0.001

emb AJ000438.1 SIAJ438	Sorex isodon partial mitochondrial c...	44	0.001
emb AJ000437.1 SIAJ437	Sorex isodon partial mitochondrial c...	44	0.001
emb AJ000428.1 SAAJ428	Sorex arcticus partial mitochondrial...	44	0.001
emb AJ000427.1 SAAJ427	Sorex arcticus ssp. maritimensis par...	44	0.001
emb AJ000426.1 SAAJ426	Sorex asper partial mitochondrial cy...	44	0.001
emb AJ000425.1 SAAJ425	Sorex asper partial mitochondrial cy...	44	0.001
emb AJ000418.1 SGAJ418	Sorex granarius partial mitochondria...	44	0.001
emb AJ000417.1 SGAJ417	Sorex granarius partial mitochondria...	44	0.001
emb AJ000416.1 SAAJ416	Sorex araneus partial mitochondrial ...	44	0.001
emb AJ004793.1 HCAJ4793	Hippolais caligata ssp. caligata mi...	44	0.001
emb AJ004792.1 HCAJ4792	Hippolais caligata ssp. rama mitoch...	44	0.001
gb U15718.1 RSU15718	Ramphocelus sanguinolentus cytochrome ...	44	0.001
gb L11905.1 CGYMTCTB3D	Cratogeomys gymnurus mitochondrial c...	44	0.001
gb U14679.1 POU14679	Philander opossum cytochrome b light s...	44	0.001
gb L11907.1 CGYMTCTB3F	Cratogeomys goldmani rubellus mitoch...	44	0.001
gb L11906.1 CGYMTCTB3E	Cratogeomys merriami mitochondrial c...	44	0.001
gb L11902.1 CGYMTCTB3A	Cratogeomys castanops castanops mito...	44	0.001
emb X92524.1 SLCYTB	S.longirostris cytochrome b gene (compl...	44	0.001
gb U46771.1 ACU46771	Anthus campestris cytochrome b gene, m...	44	0.001
dbj AB021773.1 AB021773	Anguilla interioris mitochondrial c...	44	0.001
dbj AB006953.1 AB006953	Carassius auratus langsdorfi mitoch...	44	0.001
emb Z73492.1 MTPTCTCTB	P.trochilus mitochondrial cytochrome...	44	0.001
dbj AB035239.1 AB035239	Osteoglossum ferreirai mitochondria...	44	0.001
emb X92532.1 MMCCTB2	M.monoceros cytochrome b gene (complet...	44	0.001
emb X74260.1 MIVOCYTB	V.olivaceus mitochondrion gene for cy...	44	0.001
emb X56293.1 MISLCYTB3	S.longirostris mitochondrion cytb gen...	44	0.001
emb X56292.1 MISLCYTB3A	S.longirostris mitochondrion cytb ge...	44	0.001
emb X74256.1 MIPVCYTB	P.violaceus mitochondrion gene for cy...	44	0.001
emb X82304.1 MIPFCYTB3G	P.hispida mitochondrial cytochrome b...	44	0.001
emb X82302.1 MIPFCYTB3G	P.fasciata mitochondrial cytochrome ...	44	0.001
emb X56284.1 MIOACYTB	O.aries mitochondrion cytb gene for c...	44	0.001
emb X74252.1 MIMKCYTB	M.keraudrenii mitochondrion gene for ...	44	0.001
emb X72005.1 MILWCYTB	L.weddelli mitochondrial gene for cyt...	44	0.001
emb X74259.1 MILLCYTB	L.ludovicianus mitochondrion gene for...	44	0.001
emb Y08814.1 MIHLCTB3G	H.liberiensis mitochondrial cytochro...	44	0.001
emb Y08813.1 MIHACYTB	H.amphibius mitochondrial cytochrome ...	44	0.001
emb X56287.1 MIGCCYTB	G.camelopardalis mitochondrion cytb g...	44	0.001
emb X74253.1 MIEFCYTB	E.fastuosus mitochondrion gene for cy...	44	0.001
emb X60941.1 MIACB33	Epimachus albertisii mitochondrial ge...	44	0.001
emb X74255.1 MIDMCYTB	D.magnificus mitochondrion gene for c...	44	0.001
emb X56289.1 MICHCTB	C.hircus mitochondrion cytb gene for ...	44	0.001
emb V00654.1 MI3TX	Bos taurus complete mitochondrial genome	44	0.001
emb X60940.1 MIAMCB33	A.macgregoriae mitochondrial gene for...	44	0.001
emb X92530.1 LACYTB	L.albirostris cytochrome b gene (comple...	44	0.001
gb U09265.1 CAU09265	Coccyzus americanus mitochondrion cyto...	44	0.001
dbj AB023906.1 AB023906	Petaurista leucogenys mitochondrial...	44	0.001
dbj AB023905.1 AB023905	Petaurista leucogenys mitochondrial...	44	0.001
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dbj AB023903.1 AB023903	Petaurista leucogenys mitochondrial...	44	0.001
dbj D88983.1 D88983	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88638.1 D88638	Bubalus bubalis mitochondrial DNA for c...	44	0.001
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dbj D88628.1 D88628	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D88627.1 D88627	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D84204.1 GOTMTC8D	Capra aegagrus mitochondrial DNA for ...	44	0.001
dbj D84202.1 GOTMTC8B	Capra falconeri mitochondrial DNA for...	44	0.001
dbj D82893.1 D82893	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D82892.1 D82892	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D82891.1 D82891	Bos javanicus mitochondrial DNA for cyt...	44	0.001
dbj Q12123.1 BBUMTC823	Bubalus arnee bubalis mitochondrial ...	44	0.001
dbj Q14537.1 BBUMTC8A	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj AB094974.1 AB094974	Capra hircus mitochondrial DNA for ...	44	0.001
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dbj AB094971.1 AB094971	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB094952.1 AB094952	Capra aegagrus mitochondrial DNA fo...	44	0.001
dbj D88549.1 D88549	Amos depressicollis mitochondrial DNA ...	44	0.001
dbj D88537.1 D88537	Bubalus bubalis mitochondrial DNA for c...	44	0.001

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dbj D88629.1 D88629	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D84205.1 SHPMTCBE	Sheep mitochondrial DNA for cytochrom...	44	0.001
dbj D84203.1 SHPMTCBC	Ovis musimen mitochondrial DNA for cy...	44	0.001
dbj D84201.1 GOTMTCBA	Goat mitochondrial DNA for cytochrome...	44	0.001
dbj D82894.1 D82894	Bubalus bubalis mitochondrial DNA for c...	44	0.001
dbj D82891.1 D82891	Bubalus quarlesi mitochondrial DNA for ...	44	0.001
dbj D14638.1 BBUMTCBB	Bubalus bubalis mitochondrial gene fo...	44	0.001
dbj D14636.1 BOVMTCCB	Bos javanicus mitochondrial gene for ...	44	0.001
dbj AB017602.1 AB017602	Talpa altaica mitochondrial cytb ge...	44	0.001
dbj AB018985.1 AB018985	Cichlasoma citrinellum mitochondria...	44	0.001
dbj AB004075.1 AB004075	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004073.1 AB004073	Capra hircus mitochondrial DNA for ...	44	0.001
dbj AB004070.1 AB004070	Capra hircus mitochondrial DNA for ...	44	0.001
emb X92531.1 DLCTYB	D.leucas cytochrome b gene (complete se...	44	0.001
gb U07565.1 HAU07565	Hippopotamus amphibius mitochondrion c...	44	0.001
gb U10367.1 PVU10367	Ptilonorhynchus violaceus mitochondrio...	44	0.001
gb U10364.1 CMU10364	Chlamydera maculata mitochondrion cyto...	44	0.001
emb Z96068.1 ASZ96068	Acomys spinosissimus DNA for mitochon...	42	0.005
gb U76507.1 AIU76507	Amblyornis inornatus cytochrome b gene...	40	0.021
gb AF157466.1 AF157466	Lepus timidus cytochrome b (Cyb) gen...	40	0.021
gb AF157464.1 AF157464	Lepus corsicanus haplotype 1 cytochr...	40	0.021
gb AF157463.1 AF157463	Lepus corsicanus haplotype 3 cytochr...	40	0.021
gb AY016019.1 AY016018S3	Mullerornis agilis cytochrome b ge...	40	0.021
gb AF027330.1 	Akodon olivaceus canescens museum catalog nu...	40	0.021
gb AF027329.1 	Akodon olivaceus canescens museum catalog nu...	40	0.021
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gb AF027322.1 	Akodon olivaceus beatus museum catalog numbe...	40	0.021
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gb AF027311.1 	Akodon olivaceus brachiotis museum catalog n...	40	0.021
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gb AF266188.1 AF266188	Gillichthys mirabilis cytochrome b m...	40	0.021
gb AF324034.1 AF324034	Phyllobates aurotaenia isolate Quebr...	40	0.021
gb AF272639.1 AF272639	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272636.1 AF272636	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272634.1 AF272634	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF272633.1 AF272633	Clethrionomys gapperi specimen-vouch...	40	0.021
gb AF182711.1 AF182711	Geopelia cuneata cytochrome b gene. ...	40	0.021
gb AF182587.1 AF182587	Columbina picui cytochrome b gene. P...	40	0.021
gb AF155422.1 AF155422	Sigmodon ochrognathus cytochrome b (...	40	0.021
gb AF155400.1 AF155400	Peromyscus pectoralis lacianus cyto...	40	0.021
gb AF155385.1 AF155385	Peromyscus attwateri isolate 1b cyto...	40	0.021
gb AF155384.1 AF155384	Peromyscus attwateri isolate 1a cyto...	40	0.021
gb AF155592.1 AF155592	Sigmodon ochrognathus isolate ArizAC...	40	0.021
gb AF155591.1 AF155591	Sigmodon ochrognathus isolate McLiv7...	40	0.021
gb AF155590.1 AF155590	Sigmodon ochrognathus isolate Duran4...	40	0.021
gb AF155589.1 AF155589	Sigmodon ochrognathus isolate ElmTB...	40	0.021
gb AF155588.1 AF155588	Sigmodon ochrognathus isolate Bband4...	40	0.021
gb AF133571.1 AF133571	Trachyphonus darnaudii cytochrome b ...	40	0.021
gb AF254947.1 AF254947	Ureus epileucus cytochrome b gene. Co...	40	0.021
gb AF295531.1 AF295531	Podarcis sicula cytochrome b gene. P...	40	0.021
gb AF123705.1 AF123705	Hippocampus zosterae haplotype FK.14...	40	0.021
c221NC 990994.1	Cavia porcellus complete mitochondrial genome	42	0.021

<u>gb AF004572.1 AF004572</u>	Arvicanthus niloticus cytochrome b (...)	<u>40</u>	0.021
<u>gb AF088932.1 AF088932</u>	Sminthopsis psammophila cytochrome b...	<u>40</u>	0.021
<u>gb U62697.1 ORUCYTB2</u>	Oreopholus ruficollis cytochrome b (cy...	<u>40</u>	0.021
<u>gb U62681.1 CACYTB2</u>	Charadrius australis cytochrome b (cyt ...)	<u>40</u>	0.021
<u>gb U62707.1 CVERCYTB2</u>	Charadrius veredus cytochrome b (cytb...	<u>38</u>	0.084
<u>emb AJ004315.1 HCAJ4315</u>	Hippolais caligata mitochondrial cy...	<u>38</u>	0.084

Alignments

tmpseq_0	1	cctccctagtttgcttagggattgatcg	26
<u>AF189111</u>	797	772
<u>U86834</u>	858	833
<u>AF123633</u>	56	31
<u>AF123617</u>	104	79
<u>AF127202</u>	107	82
<u>AF127194</u>	107	82
<u>AF217828</u>	845	820
<u>AF160578</u>	869	844
<u>AF009931</u>	869	844
<u>AF091629</u>	869	844
<u>AF034967</u>	869	844
<u>AF038290</u>	869	844
<u>U07577</u>	869	844
<u>U81343</u>	791	766
<u>AJ222681</u>	869	844
<u>M99464</u>	869	844
<u>AJ225116</u>	869	844
<u>U25738</u>	872	847
<u>U25736</u>	872	847
<u>U15202</u>	872	847
<u>U15204</u>	872	847
<u>X56290</u>	869	844
<u>X56286</u>	869	844
<u>D88639</u>	869	844
<u>D82890</u>	869	844
<u>AF119261</u>	869	847
<u>AF123615</u>	101	79
<u>AF160603</u>	866	844
<u>U62687</u>	179	157
<u>U62685</u>	179	157
<u>AF022071</u>	866	844
<u>AF022070</u>	866	844
<u>U81317</u>	872	850
<u>U37293</u>	774	752
<u>U37292</u>	774	752
<u>U37291</u>	774	752
<u>AF082055</u>	51	29
<u>U72770</u>	798	776
<u>U07578</u>	869	847
<u>AF031908</u>	187	165
<u>AJ004231</u>	773	751
<u>AJ004230</u>	773	751
<u>AJ004229</u>	773	751
<u>AJ004232</u>	773	751
<u>U88865</u>	850	828
<u>U90001</u>	536	514
<u>U63057</u>	773	751
<u>AB036404</u>	173	151
<u>AB036402</u>	173	151
<u>AB036400</u>	173	151
<u>AB036398</u>	173	151
<u>U19611</u>	774	752
<u>K22539</u>	869	847
<u>L08014</u>	872	850
<u>L08011</u>	872	850
<u>AX016012</u>	11937	11912
<u>AF974591</u>	677	652
<u>AX003212</u>	761	736
<u>AX005211</u>	761	736
<u>AF182133</u>	797	772
<u>AF182130</u>	797	772

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<u>AF189117</u>	797a.....	772
<u>AF189116</u>	797g.....	772
<u>AF112140</u>	310g.....	285
<u>AF112139</u>	310g.....	285
<u>AF112138</u>	310g.....	285
<u>AF081990</u>	872c.....	847
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<u>AF081964</u>	872c.....	847
<u>AF081962</u>	754c.....	729
<u>AF081961</u>	872c.....	847
<u>AF081960</u>	872g.....	847
<u>AF081959</u>	872c.....	847
<u>AF112405</u>	869c.....	844
<u>AF144317</u>	161g.....	136
<u>AF144316</u>	161g.....	136
<u>AF144315</u>	161g.....	136
<u>AF144314</u>	161g.....	136
<u>AF144313</u>	161g.....	136
<u>AF144312</u>	161g.....	136
<u>AF144311</u>	161g.....	136
<u>AF144310</u>	161g.....	136
<u>AF144309</u>	161g.....	136
<u>NC 001567</u>	15382g.....	15357
<u>AF212124</u>	425c.....	400
<u>AF182706</u>	739a.....	714
<u>AF010406</u>	15027a.....	15002
<u>AF096452</u>	735c.....	710
<u>AF283619</u>	845a.....	820
<u>AF283618</u>	845a.....	820
<u>AF283608</u>	845a.....	820
<u>AF283602</u>	845a.....	820
<u>AF110069</u>	770a.....	745
<u>AF146616</u>	95g.....	70
<u>AF271410</u>	869g.....	844
<u>AF290139</u>	752g.....	727
<u>NC 002504</u>	15022g.....	14997
<u>AF163901</u>	869g.....	844
<u>AF119261</u>	869g.....	844
<u>AF119259</u>	869g.....	844
<u>AF288454</u>	91a.....	66
<u>AF163875</u>	869c.....	844
<u>AF123642</u>	68g.....	43
<u>AF123647</u>	68g.....	43
<u>AF123646</u>	104g.....	77
<u>AF123643</u>	68g.....	43
<u>AF123644</u>	64g.....	39

	c.....	79
<u>AF123628</u>	104g.....	79
<u>AF123621</u>	85g.....	60
<u>AF123619</u>	104g.....	79
<u>AF123618</u>	104g.....	79
<u>AF123614</u>	104g.....	79
<u>AF123611</u>	101g.....	76
<u>AF127201</u>	107g.....	82
<u>AF127192</u>	107t.....	82
<u>AF127189</u>	107g.....	82
<u>AF197849</u>	872g.....	847
<u>AF197847</u>	872t.....	847
<u>NC 000889</u>	15040g.....	15015
<u>NC 002079</u>	16164g.....	16119
<u>NC 001794</u>	15052a.....	15027
<u>NC 001610</u>	15045t.....	15020
<u>AF201612</u>	520t.....	495
<u>AF097931</u>	869a.....	844
<u>AF097927</u>	869g.....	844
<u>J01394</u>	15382g.....	15357
<u>AF168760</u>	507a.....	482
<u>AF168759</u>	507a.....	482
<u>AF168758</u>	507a.....	482
<u>AF168756</u>	507a.....	482
<u>AF182381</u>	692t.....	667
<u>AF182380</u>	692t.....	667
<u>U89187</u>	872a.....	847
<u>AF193833</u>	773g.....	748
<u>AF193822</u>	773g.....	748
<u>AF193821</u>	773a.....	748
<u>AF217837</u>	845t.....	820
<u>AF217835</u>	845t.....	820
<u>AF217834</u>	845a.....	820
<u>AF217831</u>	845g.....	820
<u>AF217823</u>	845a.....	820
<u>AF217819</u>	845a.....	820
<u>AF217815</u>	845c.....	820
<u>AF118156</u>	101g.....	76
<u>AF209938</u>	418a.....	393
<u>AF209933</u>	418a.....	393
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<u>U88857</u>	863g.....	818
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<u>AJ000438</u>	740a.....	715
<u>AJ000437</u>	740a.....	715
<u>AJ000428</u>	740a.....	715
<u>AJ000427</u>	740a.....	715
<u>AJ000426</u>	740g.....	715
<u>AJ000425</u>	740g.....	715
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<u>Q88627</u>	869a.....	844
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<u>Q82822</u>	869a.....	844
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<u>AF157466</u>	791	772
<u>AF157464</u>	793	774
<u>AF157463</u>	793	774
<u>AY016019</u>	93	74
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<u>AF027307</u>	869	850
<u>AF266188</u>	371	352
<u>AF324034</u>	408	389
<u>AF272639</u>	869	850
<u>AF272636</u>	869	850
<u>AF272634</u>	869	850
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<u>AF182711</u>	712	693
<u>AF182687</u>	774	755
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<u>AF155409</u>	869	850
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<u>AF155588</u>	869	850
<u>AF121511</u>	771	752
<u>AF264047</u>	869	850
<u>AF206531</u>	771	752
<u>AF192706</u>	863	844
<u>NC 000884</u>	15032	15013
<u>AF004572</u>	869	850
<u>AF088912</u>	869	850
<u>U62697</u>	176	157
<u>U62681</u>	179	160
<u>U62707</u>	179g.....n..	154
<u>AJ004315</u>	773t.....n.....	748

Database: nt

Posted date: Mar 2, 2001 12:20 AM

Number of letters in database: 2,863,827,885

Number of sequences in database: 807,597

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 19068

Number of Sequences: 807597

Number of extensions: 19068

Number of successful extensions: 7580

Number of sequences better than 10.0: 2441

length of query: 26

length of database: 2,863,827,885

effective RSP length: 17

effective length of query: 9

effective length of database: 2,850,098,736

effective search space: 25650888624

effective search space used: 25650888624

T: 0

A: 30

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 16 (32.2 bits)

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no1
21	weaver bird no2
22	buffalo no1
23	buffalo no 2

CLAIMS

- 1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	Sequence (5'-3')
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTTGTAGGGATTGATCG"

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:
- Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*:
- "taccatgaggacaaatatcttttgaggagcaacagtcacccaatctccttcagcaatcccatacatcggtacaaacctag tagaatgaatctgaggagggtctcagtagataaagcaacccttaccgattttcgccttcactttatcctccatttatcattgc agcccttaccatagtagacactactgtttctccacgaaacaggatccaacaacccacaggaatctcatcagacgcagacaaa attccattccaccctactacactatcaagatatcttaggagctctactattaattttaaccctcatgcttctagtctattctcacc ggacctgcttgagacccagacaactataaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttc ctatttcatacgcgaatcctccgatcaattcctaacaactaggagg"
6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
- isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
 - sequencing the amplified products,
 - blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample,

- d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,
- 5 e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,
- f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,
- 10 g) aligning the sequences obtained using CLUSTAL program and identifying the variable sites amongst the animals analyzed,
- h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.
- 15
7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.
- 20
8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 μ l reaction volume containing approximately 20 ng of template DNA, 100 μ M each of dNTPs, 1.25 pmole of each primer, 1.5mM MgCl₂, 0.5 unit of AmpliTaq Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95°C for 10 min, followed by 35 cycles each of denaturation at 95°C for 45 s, annealing at 51°C for 1 min, and extension at 72°C for 2 min. The extension step at 35th cycles should be held for 10 min.
- 25
9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.
- 30
10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.
11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

- 5 12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
- 10 14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
- 15 15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wantedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
- 20 16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECULAR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.

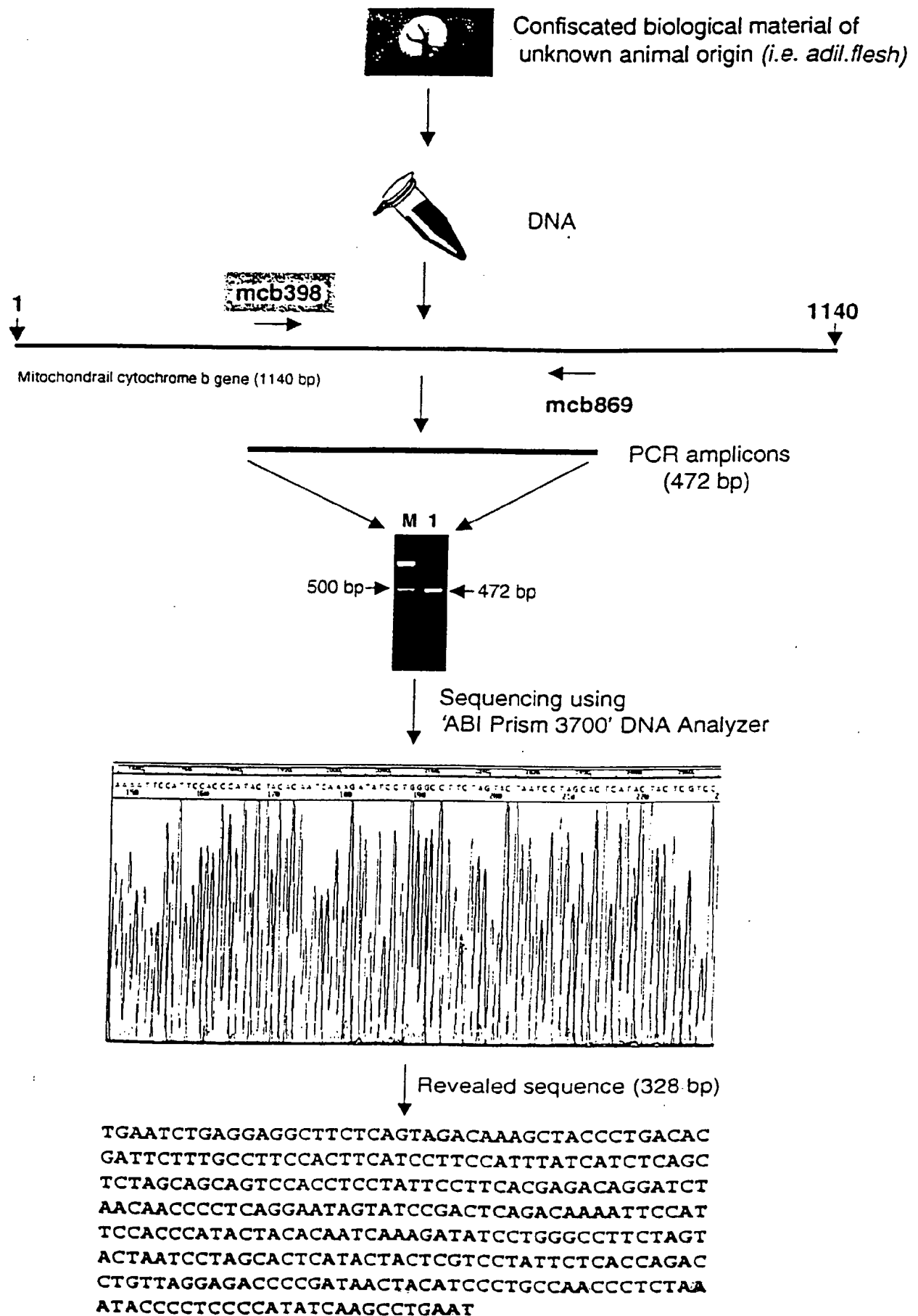
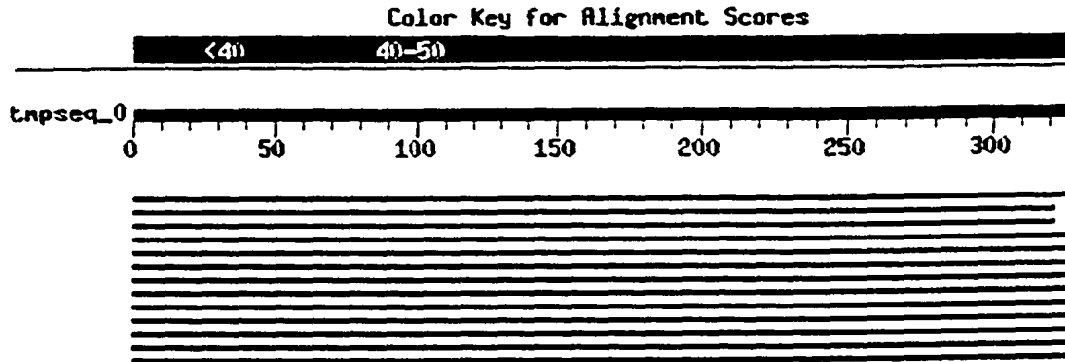


Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers 'mcb398' and 'mcb869'

Homology search in 'nr' database using 'BLAST'

<http://www.ncbi.nlm.nih.gov/BLAST/>



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information
and further analysis using primers 'mcb398' and 'mcb869'

Multiple sequence alignments
using 'Autoassembler'

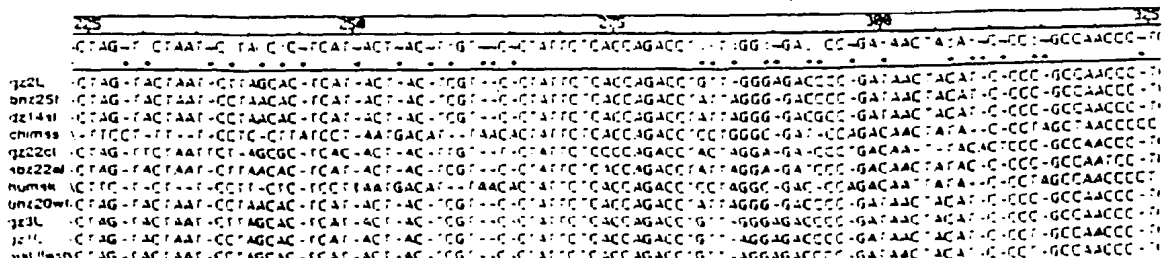


Figure 1 b

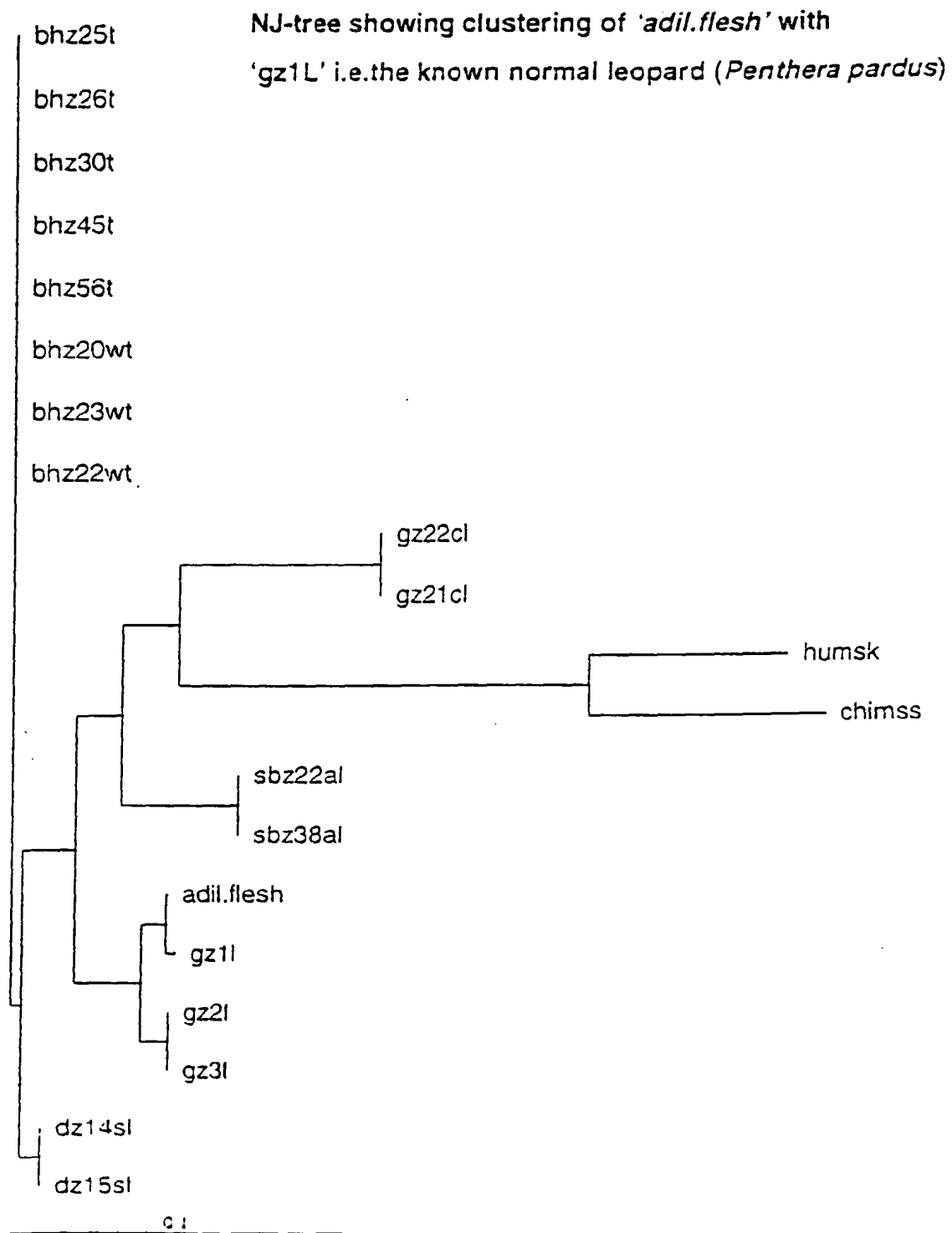


Figure 1c

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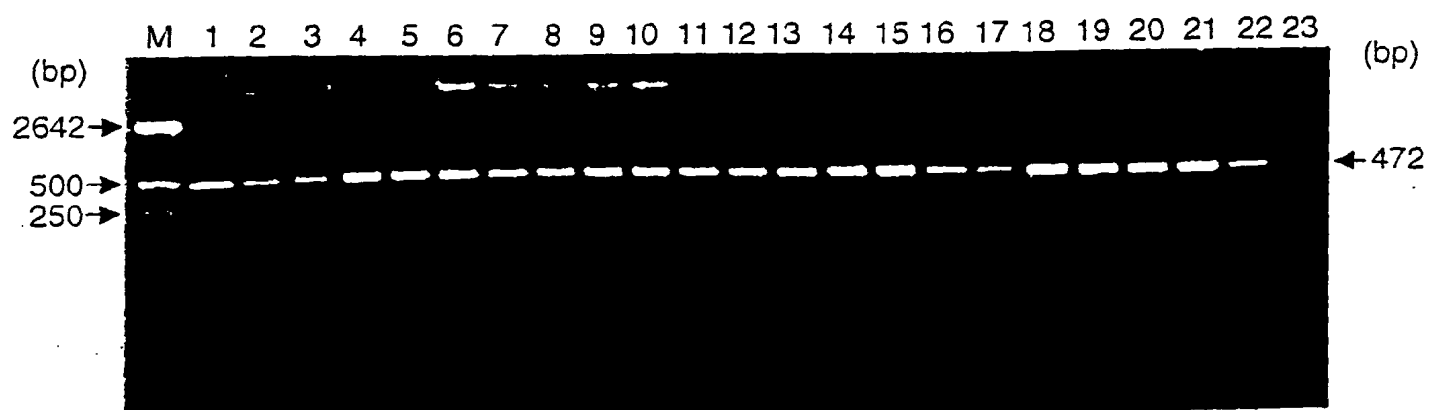


Figure 2

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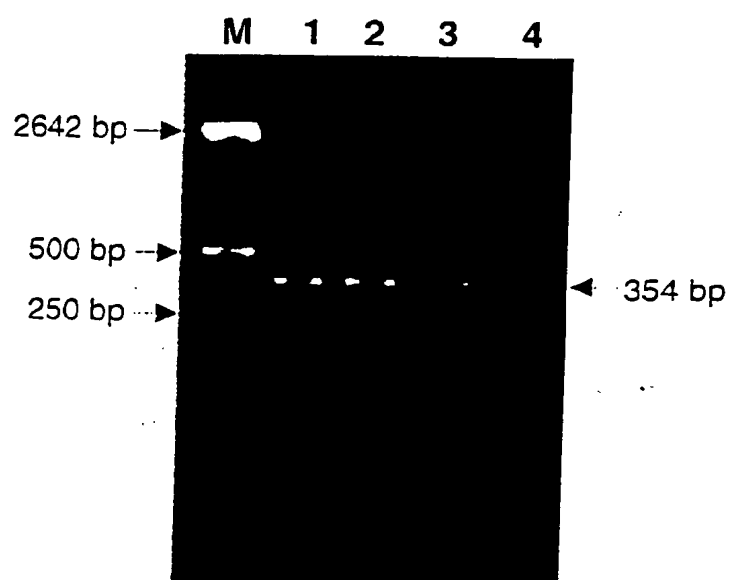


Figure 3

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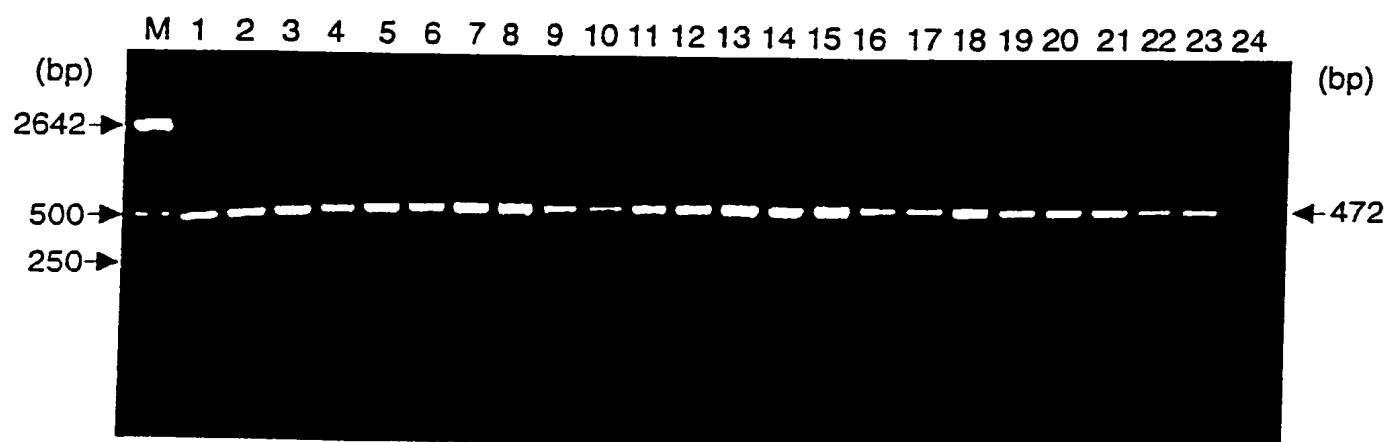


Figure 4

INTERNATIONAL SEARCH REPORT

Inte Application No
PC 1 / IN 01/00055

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document	1-16

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

° Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *G* document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

12/03/2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/JP 01/00055

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	WO 93 15215 A (HYDROCARBON RESEARCH INC) 5 August 1993 (1993-08-05) the whole document ----	1-16
Y	EP 0 807 690 A (KARL SCHMITZ SCHOLL FONDS FUER) 19 November 1997 (1997-11-19) the whole document ----	1-16
Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document ----	1-16
Y	SHANKARANARAYANAN PATTABHIRAMAN ET AL: "Mitochondrial DNA sequence divergence among big cats and their hybrids." CURRENT SCIENCE (BANGALORE), vol. 75, no. 9, 10 November 1998 (1998-11-10), pages 919-923, XP001063942 ISSN: 0011-3891 the whole document ----	1-16
A	THOMPSON JULIE D ET AL: "A comprehensive comparison of multiple sequence alignment programs." NUCLEIC ACIDS RESEARCH, vol. 27, no. 13, 1 July 1999 (1999-07-01), pages 2682-2690, XP002191669 ISSN: 0305-1048 the whole document -----	

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			EP 0807690 A1	19-11-1997
			WO 9743618 A2	20-11-1997
